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OM protein - protein search, using sw model

December 2, 2002, 06:48:57; Search time 30.9427 Seconds (without alignments) 1363.907 Million cell updates/sec Run on:

US-09-902-563-2 2378 Title: Perfect score:

1 MKLANWYWLSSAVLATYGFL.....GYKSSFKEAKMMIRPKHFKP 439 Scoring table: BLOSUM62 Gapoxt 0.5 Sequence:

283224 seqs, 96134422 residues Searched:

al number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result No.	Score	Query Match	Length	DB		Description
1	2378	100.0	439	. 2	I37391	fibrinogen-like pr
7	1853.5	77.9	432	7	A27447	cytotoxic T-lympho
3	1849.5	77.8	432	7	156934	fibrinogen-like pr
4	511.5	21.5	463	7	A38463	fibrinogen beta ch
22	506.5	21.3	312	7	JN0596	
9	484.5	20.4		Н	FGHUGB	fibrinogen gamma-B
7	480.5	20.2	437	Н	FGHUG	fibrinogen gamma-A
80	479.5	20.2	479	7	A25052	fibrinogen beta ch
σ	470	19.8	468	7	FGBOB	
10	462	19.4	444	7	805313	fibrinogen gamma-B
11	461	19.4	491		FGHUB	
12	456	19.2	438		A32670	fibrinogen gamma c
13	452		334		JC5980	
14	451	19.0	998		D44234	fibrinogen alpha c
15	446		282		A35084	fibrinogen-related
16	434.5	18.3	326		B47172	ficolin-beta - pig
17	431	18.1	328	7	A05299	fibrinogen beta ch
18	428.5	18.0			A47172	transforming growt
19	428.5	18.0			FGLMGS	fibrinogen gamma c
20	423	17.8			S61517	ficolin-1 precurso
21	423	17.8			JH0675	restrictin precurs
22	417.5	17.6			A45445	janusin precursor,
23	404	17.0			FGRTGA	fibrinogen gamma-A
24	404	17	445		FGRTGB	fibrinogen gamma-B
25	403.5	1			S28170	tenascin homolog -
26	403.5	17.0			S65944	tenascin-X - pig (
27	401.5	~	4		T42629	tenascin-X - bovin
28	397.5	16.7	3566		^	
29	396	16.7	2019	J	JQ1322	tenascin precursor

421 YKSSFKEAKMMIRPKHFKP 439

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tenascin-X - mouse	probable tenascin	tenascin-C - human	tenascin precursor	tenascin precursor	tenascin Y precurs	fibrinogen alpha-I	scabrous locus (sc	hypothetical prote	hypothetical prote	hypothetical prote	microfibril-associ	hypothetical prote	hypothetical prote		cytotactin - chick
148839	T09070	A32160	S19694	A32230	T42635	A41932	A39832	T15876	T21773	121772	PC2036	T32255	T29850	T26827	A31930
7	7	7	,	П	7	H	7	7	7	7	7	7	7	7	7
860	4006	2201	1746	1810	1914	641	774	463	915	927	127	146	431	452	933
16.5	16.5	16.3	16.3	16.2	16.1	15.0	14.6	9.1	8.3	8.3	7.8	6.7	6.7	6.7	5.9
393.5	393.5	388	386.5	386	382.5	356.5	346.5	215.5	198	198	184.5	160	160	160	140
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 fibrinogen-like protein expressed in T lymphocytes (pT49) - human fibrinogen-like protein expressed in T lymphocytes (pT49) - human fishers: Homo sapiens (man) fishers: Homo sapiens (man) fishers: Homo sapiens (man) fishers: Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000 C.Accession: 137391; S47273 Fishers: Sapiens fishers Rene 160, 257-262, 1995 A.Tritle: Sequence of a human transcript expressed in T-lymphocytes and encoding a fib	inumber: in 137391 reliminantype: mRt 1-439 ferences: erences: mitted to	Ouery Match 100.0%; Score 2378; DB 2; Length 439; Best Local Similarity 100.0%; Pred. No. 4.3e-157; Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 MKLANWYWI.SSAVLATYGELVVANNETEBIKDERAKDVCPVRLESRGKCEBAGECPYQVS 60 	1 LPPLTIQLPKQFSR1EEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG 120 	1 APGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANL 180 	1 TFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEV 240	1 YCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMIL 300 	1 RIDLEDFRGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPD 360 	1 KDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHOKYRGVRNGIFWGTWPQVSEAHPGG 420
RESULT 1 137391 fibrinoger C; Species C; Acte: 0 C; Accessic R; Ruegg, 0 Gene 160, A;Title: 3	A; Reference A; Accession A; Status: p A; Molecule A; Residues: A; Cross-ref A; Cross-ref C; Superfami F; 210-435/E	Query Match Best Local Matches 43	ਜ ਜ	61	121	181	241	301	361
RES 137 137 C; S C; S C; S Ger A; T	FCAPAPA	O H Z	Qy Db	QY	Qy	QY Db	QY	QY	QY

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C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disu F;73-202/Domain: fibrinogen disulfide ring homology <PR>F;212-460/Domain: fibrinogen beta/gamma homology <PBG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage A;Reference number: A38463; MUID:91182745; PMID:2009266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Gallus gallus (chicken)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change_13-Aug-1999
C:Accession: A38463
R:Welssbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
Biochemistry 30, 3290-3294, 1991
                                                                                                                                                                                                                                                                                                                                                   61 LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG 120
                                                                                                                                                                                                                                                                                                                                                                                          59 LPTLTIQLPRQLGSMEEVLKEVRTLKEAVDSLKKSCQDCKLQADDHRDPGGNG----GNG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 APGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 TEVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 YCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMIL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 RIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 KDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVRNGIFWGTWPGVSEAHPGG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Gaps
                                                                                                                                                                                                                                                                               1 MKLANWYWLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 VAKFSDISTIMYQYVNMIDNKLVKTQKQRKD-----NDIILSEYNTEMELHYNYIK--D 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 QDKQAMKKGPIIYPDAGGCKHPLDELGVLCPTGCE---LQTTLLKQEKTVKPVLRDLKDR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 ------LKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVRELE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB:M58514; NID:g211779; PIDN:AAA48770.1; PID:g211780
                         A;Gene: musfiblp
C;Superfamlly: fibrinogen gamma chain; fibrinogen beta/gamma homology
F;203-428/Domain: fibrinogen beta/gamma homology <FBG>
                                                                                                                                                DB 2; Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71; Mismatches 154; Indels 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 463;
                                                                                                                                                                                                     Indels
                                                                                                                                          77.8%; Score 1849.5; DB 2 77.4%; Pred. No. 1.6e-120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.5%; Score 511.5; DB 2 30.4%; Pred. No. 7.8e-28;
                                                                                                                                                                                                42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fibrinogen beta chain - chicken (fragment)
                                                                                                                                                                   Best Local Similarity 77.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 YKSSFKEAKMMIRPKHFKP 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414 YKSSFKQAKMMIRPKNFKP 432
                                                                                                                                                                                             Matches 340; Conservative
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A; Residues: 1-463 <WEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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                                                                                                                                                Query Match
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              C; Genetics:
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                                                                                                                                                                                                                                                     R;Koyama, T.; Hall, L.R.; Haser, W.G.; Tonegawa, S.; Saito, H. Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987
A;Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology to A;Reference number: A27447; MUID:87175527; PMID:3550794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.Parr, R.L.; Fung, L.; Reneker, J.; Myers-Mason, N.; Leibowitz, J.L.; Levy, G. J. Virol. 69, 5033-5038, 1995
A.Title: Association of mouse fibrinogen-like protein with murine hepatitis virus-induce A; Reference number: 156934; MUID:95333285; PMID:7609073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                cytotoxic T-lymphocyte-specific protein precursor (clone pT49) - mouse C; Species: Mus musculus (house mouse) C; Date: 15-Dec.1988 #sequence_revision 15-Dec-1988 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fibrinogen-like protein - mouse
C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 APGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 AE-TAEDSRVQELESQVNKLSSELKNAKDQIQGLQGRLETLHLVNMNNIENYVDNKVANL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 YCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMIL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLANWYWLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 KDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVRNGIFWGTWPGVSEAHPGG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-432 <RES>
A;Cross-references: GB:S78773; NID:91042169; PIDN:AAB34823.1; PID:91042170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Cross references: GB:M16238; NID:g193304; PIDN:AAA37624.1; PID:g387156 C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology L;203.428/Domain: fibrinogen beta/gamma homology <FBG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 1853.5; DB 2; Length; Pred. No. 8.6e-121; 42; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                   421 YKSSFKEAKMMIRPKHFKP 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.98;
77.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 YKSSFKEAKMMIRPKHFKP 439
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Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-432 <KOY>
                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
                                                                                                                                                                                                                                  C; Accession: A27447
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0y 135 SEVNKLSSELKNAKEEINVLHGRLEKILLVNNNNNIENVUSEKVANLTFVVNSLDGKCSKC Db 160 NIDDNIPSSILKVLRAVIDSLHKKIQKLENAIATOTDYCRSEC OY 195 PSQEQIOGRPVQHLIYKDCSDYYAIGKRSETYRYPDPKNSSFEVYCDMETMGGGWTLI Db 202VASCNIPVSGRECEDIYRKGGETSEMYIIQPDPFTTPYRVYCDMETMGGGWTLI OY 255 QARLDGSTWFTRTQDYRAGFGRIRR	188 73 248 117	117 305 1177 359 237 418
0y 135 SEVNKLSSELKNA 0y 195 PSQEQIOSRPVQH 0b 202VASCNIPY 0y 255 QARLDGSTRFTR 0b 205VASCNIPY 0y 255 QARLDGSTRFTR 0b 304 LEDFNGVELYALX 1 1 1 1 1 0b 317 MEDWNGDKYSALY 0y 355 FFTTPDKDNDRY- 0b 317 WEDWNGDKYSALY 0y 355 FFTTPDKDNDRY- 0b 317 WFSTYDRDNDGWL 0b 317 WFSTYDRUDGWL 0b 317 WFSTYDRUGWL 0b 317 WFSTYDRUDGWL 0b 317 WFS	129 FVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANLTFVVNSLD : : : :	GGWTVLQARLDGSTNFTRT GGWTVLQARLDGSTNFTRT GGWTVIORRSDGSENFNRG DFNGVELYALYDGFVANE DFNGVELYALYDGFVANE DFNGVELYALYDGFVANE DFNGVELYALYDGFVANE 1 1 1 1 1 1 1

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Residues: 1-113,'T',115-453 <RIX>
Loss-references: GB:M10014; GB:J00134; GB:J00135; GB:X00086; NID:g182438; PIDN:AAB
Pornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
Bloil. Chem. 259, 12826-12830, 1984
Litle: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near t
Reference number: A92448; MUID:85030379; PMID:6092346
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Ittle: Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain varia
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Tross references: EMBL:X51473; NID:q31410; PIDN:CAA35837.1; PID:g930064

Comment: The two forms of gamma chain, A (see PIR:FGHUG) and B, arise by alternate con, which makes this chain different from the gamma-B chain at positions 434-437 a comment: The gamma-B chain is present in about 10% of the fibrinogen molecules in p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tancis, C.W.; Musller, E.; Henschen, A.; Simpson, P.J.; Marder, V.J.
Tancis, C.W.; Musller, E.; Henschen, A.; Simpson, P.J.; Marder, V.J.
Toc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988
Litle: Carboxyl-terminal amino acid sequences of two variant forms of the gamma-cha veference number: A94194; MUID:88217900; PMID:3368448
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upperfamily: fibrinogen beta/gamma homology
upperfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
ieywords: alternative splicing; blood coagulation; calcium; colled coil; glycoprote
-26/Domain: signal sequence #status predicted <SIG>
-76/37/Product: fibrinogen gamma-B chain #status experimental <MPT>
-76-415/Domain: fibrinogen beta/gamma homology <FBG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F341.355/Domain: calcium binding #status predicted <CRB>
F340.422/Region: polymerization site, binding to the amino end of the alpha chain of F340-422/Region: polymerization site, binding to the amino end of the alpha chain of F34/Disulfide bonds: interchain (to gamma 35) #status predicted F35/Disulfide bonds: interchain (to beta-110) #status predicted
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Residues: 411-434,'Y',436-440,'Z',442,'Z',444,'B',446-447,'R',449,'ZBB',453 <WOL>
                                                                                                                                                                                                                                                       Species: Homo sapiens (man)

Mar. 1987 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #1242 #12
                                                                                                             orinogen gamma-B chain precursor [validated] - human
ulternate names: coagulation factor I; fibrinogen gamma-55 chain
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Agrichett, L.; Zanelli, T.; Malcovati, M.; Tenchini, M.L. A Seq. 1, 419-422. 1991
fitle: Polymorphism of the human gamma chain fibrinogen gene. Reference number: 137390; MUID:92119334; PMID:1685103
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RiFornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R. J. Biol. Chem. 259, 12826-12830, 1984
A; Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near thiseference number: A92448; MUID:85030379; PMID:6092346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Bertgonolli, M.E.; Beckerle, M.C.
J. Cell Biol. 121, 1329-1342, 1937
A;Title: Evidence for the selective association of a subpopulation of GPIIb-IIIa with A;Reference number: A40698; MUID:93286185; PMID:8509453
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A; Residues: 27-33, XX, 36-41 <BER>
A; Experimental source: throubin-activated platelets
A; Note: sequence extracted from NCBI backbone (NCBIP:133734)
R; Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
B; Chemistry 33, 1988-1993, 1994
A; Title: Identification of proteins associated with apolipoprotein A-I-containing lip
A; Reference number: A54223; MUID:94162201; PMID:8117655
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R;Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1376
A;Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A;Reference number: A94309; MUID:76225080; PMID:936108
A;Contents: annotation; disulfide bonds
R;Hoeprich, PD.; Doolittle, R.F.
Biochemistry 22, 2049-2055, 1883
A;Title: Dimeric half-molecules of human fibrinogen are joined through disulfide bond
A;Residues: 27-437 <HEN>
R;Rant, J.A.; Lord, S.T.; Crabtree, G.R.
Proc. Natl. Acada Sci. US.A. 80, 3953-3957, 1983
A;Title: Partial mRNA sequences for human Aalpha, Bbeta, and gamma fibrinogen chains: A;Reference number: A93956; MUID:83247396; PMID:6575389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 286-437 <FOR>
R:Imam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.
Nucleic Acids Res. 11, 7427-7434, 1983
A; Title: Isolation and characterisation of cDNA clones for the Aalpha- and gamma-chai
A; Reference number: I37393; MUID:84069777; PMID:6689067
A; Accession: I37393
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R; Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrall, B.A.; Cassman, K.G.
R; Begulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., F
A; Title: The structures of fibrinogen and fibrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Contents: annotation; review, EM structure, polymerization, ligands
R;Horwitz, B.H.; Varadi, A.; Scheraga, H.A.
Proc. Natl. Acad. Sci. U.S.A. al, 580-5984, 1984
A;Title: Localization of a fibrin gamma-chain polymerization site within segment Thr-A;Reference number: A94006; MUID:85014892; PMID:6592597
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A;Residues: 27-33, XX',36-41 <KUN>
A;Note: identification of tryptic peptides from high-density lipoproteins
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A.Contents: annotation; quaternary structure, disulfide bonds
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A;Title: Covalent structure of fibrinogen.
A;Reference number: A90037; MUID:83254370; PMID:6575689
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A;Title: Fibrinogen and fibrin.
A;Reference number: A90041; MUID:84305751; PMID:6383194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 209-270 <RES>
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                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 276-437 <KAN>
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A.Alternate names: coagulation factor I

C.Species: Homo saptens (man)

R.Species: Homo saptens (man)

R.Species: Homo saptens (man)

R.Species: Homo saptens (man)

A.Title: Characterization of a complementary deoxyribonucleic acid coding for the gamma A.Reference number: A90470; MUID: 82283444; PMID: 6688357
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A; Cross-references: GB:X02415; GB:M10014; NID:g182438; PIDN:AAB59531.1; PID:g182439
B; Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
in Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56, PA; Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural A; Reference number: A94433
    F;49/Disulfide bonds: interchain (to alpha-64) #status predicted F;78/Bainding site: carbohydrate (Asn) (covalent) #status predicted F;161/Disulfide bonds: interchain (to beta-227) #status predicted F;165/Disulfide bonds: interchain (to alpha-180) #status predicted F;179-208,322-386/Disulfide bonds: #status predicted F;179-208,322-386/Disulfide bonds: #status predicted F;474/Cross-link: isopeptide (Gln) (interchain to Lys-422 N6-amino) #status predicted F;432/Cross-link: isopeptide (Lys) (interchain to Gln-424) #status predicted
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Biochemistry 24, 2077-2086, 1985
A;Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A;Reference number: A90494; MUID:85252774; PMID:2990550
A;Accession: B90494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 VDKDLQSLEDILHQVENKTSEVKQLIKAIQ-LTYNPDESSKPNMI------DAAT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 EAQCQE-PCKDTVQ---IHDITGKDCQDIANKGAKQSGLYFIKPLKANQQFLVYCEIDGS 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 GGGWTVLQARLDGSTNFTRTWQDYKAGFGNL----RREFWLGNDKIHLLTKSKEM--ILR 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 GNGWTVFQKRLDGSVDFKKNWIQYKEGFGHLSPTGTTEFWLGNEKIHLISTQSAIPYALR 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 IDLEDFNGVELYALYDQFYVANEFLKYRLHVGNY-NGTAGDAL-RFNKHYNHDLKFFT-- 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 -----TPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYH------QKYRGVRNG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 NGMQFSTWDNDNDKF-EGNCAEQDGSGWWMNKCHAGHINGVYYQGGTYSKASTPNGYDNG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 LPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 NRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANLTFVVNSL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 LKSRKMLEEIMKYEASILTHDSSIRYLQ-----EIYNSNN-----QKIVNLKEKVAQL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 DGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETM 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 WLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVSLPPLTIQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 FLSSTCVA-----YVATRDNCCILDERFGSYCPT------TCGIADFLSTYQTK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405 IFWCTWP-------GVSEA---HPGGYKSSFKEAKMMIRPKH 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 IIWATWKTRWYSMKKTTMKIIPFNRLTIGEGQQHHLGGAK------QVRPEH 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66
                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 453;
                                                                                                                                                                                                                                                                                                                                                                          20.4%; Score 484.5; DB 1; Length 4 29.7%; Pred. No. 5.6e-26; tive 56; Mismatches 178; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-437 <CHU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 141;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Ricottrell, B.A.; Doolittle, R.F.
Blochim. Biophys. Acta 453, 426-438, 1976
A;Title: Amino acid sequences of lamprey fibrinopeptides A and B and characterization
A;Reference number: A03120; MUID:77065679; PMID:999898
A;Accession: A03124
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C;Keywords: blood coagulation; glycoprotein; sulfoprotein
F;l-36/Product: fibrinopeptide B #status experimental <FPB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Petromyzon marinus (sea lamprey)
C;Date: 25-Oct-1887 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
C;Accession: A2552; A0124; B3124
R;Bohonus, V.L.; Doolittle, R.F.; Pontes, M.; Strong, D.D.
Biochemistry 25, 6512-6516, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 CTVNCRVPVVSGMHCEDIYRNGGRTSEAYYIQPDLFSEPYKVFCDMESHGGGWTVVQNRV 277
                    302 IDLEDFNGVELYALYDQFYVANEFLKYRLHVGNY-NGTAGDAL-RFNKHYNHDLKFFT-- 357
                                                                                                                                                                                                                                                                                                                                                                                                                                          274 VELEDWNGRISTADYAMFKVGPEADKYRLTYAYFAGGDAGDAFDGFDFGDDPSDKFFTSH 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 ELREELLKQRDPVR------QKISMLK-------QKISMLK-------QKISWLYF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 VNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVRELESEVNKLSSELKNAK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 INSFDR------MASDSNTLKQN-------VQTLRRRLNSRSSTHVNAQ 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 KEI---ENRYKEVKI----RIESTVAGSLRSMKSVLEHLRAKMQRMEEAIKTQKELCSAP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 -----VOHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLOARL 258
                                                                                                                                                    248 GGGWTVLQARLDGSTNFTRTWQDYKAGFGNL----RREFWLGNDKIHLLTKSKEM--ILR 301
                                                                                                                                                                                                                                                 214 GNGWTVFQKRLDGSVDFKKNWIQYKEGFGHLSPTGTTEFWLGNEKIHLISTQSAIPYALR 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 -----TPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYH------QKYRGVRNG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66; Mismatches 138; Indels 113; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 EIKDERAKDVCPVRLESRGKCEEAGECPYQVSLPPLTIQLPKQFSRIEEVFKEVQNLKEI 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB:M14773; NID:g213191; PIDN:AAA49261.1; PID:g213192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Complementary DNA sequence of lamprey fibrinogen beta chain. A; Reference number: A25052; MUID:87076582; PMID:3790537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;229-477/Domain: fibrinogen beta/gamma homology <FBG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibrinogen beta chain - sea lamprey (fragments) N;Contains: fibrinopeptide B
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A:Residues: 1-36 <COT1>
A:Accession: B03124
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A; Residues: 39-479 <BOH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A25052
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C; Superfamily: fibringen gamma chin; fibringen beta/gamma homology
C; Keyords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein;
C; Keyords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein;
E; 1-26/Domain: signal sequence #status predicted <SIG>
F; 7-43/Protouct: fibrinogen gamma-A chain #status experimental <MPT>
F; 176-415/Domain: dibrinogen beta/gamma homology crBG>
F; 341-355/Domain: calcium binding #status predicted <CAB>
F; 341-355/Domain: calcium binding #status predicted <AB>
F; 341-355/Domain: calcium binding #status predicted <AB>
F; 341-355/Domain: calcium binding #status experimental
F; 357/Disulfide bonds: interchain (to gamma-35) #status experimental
F; 357/Disulfide bonds: interchain (to beta-110) #status experimental
F; 357/Disulfide bonds: interchain (to beta-227) #status experimental
F; 57/Disulfide bonds: interchain (to beta-227) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;179-208,352-365/Disulfide bonds: *status experimental F;424/Cross-link: isopeptide (Gln) (interchain to Lys-432 N6-amino) *status experimental F;432/Cross-link: isopeptide (Lys) (interchain to Gln-424) *status experimental
A;Title:'Platelet receptor recognition site on human fibrinogen. Synthesis and structure A;Reference number: A90483; MUID:6420545; PMID:6326808 A;Contents: annotation; platelet aggregation region R;Plow, E.F.; Srouji, A.H.; Mayer, D.; Marguerie, G.; Ginsberg, M.H. J. Biol. Chem. 259, 5388-5391, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jer) and between alpha chains (weaker) of different monomers. S. Comment: All fibrinogen chains are synthesized in the liver. C. Comment: The two forms of gamma chain, A and B (see PIR:FGHUGB), arise by alternate spintron, which makes this chain different from the gamma-B chain at positions 434-437 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introps: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1; 433/3
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FG ins are contained in the core. Two three-chain colled coils emerge from this core and co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: Localization of a fibrinogen calcium binding site between gamma-subunit positid
A,Reference number: A92549; MUID:85261382; PMID:3160702
A,Contents: annotation; calcium binding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-te
A;Reference number: A37117; MUID:90337977; PMID:2143188
A;Contents: annotation; hementin cleavage site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: hementin, a protease from Haementeria ghilianii, the giant South American leech, comment: The conversion of fibriniogen to fibrin is triggered by thrombin, which cleave ation sites responsible for the formation of the soft clot.
Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
                                                                                                                                                                                   J. Biol. Chem. 259, 5388-5391, 1984
A.Title: Evidence that three adhesive proteins interact with a common recognition site A.Reference number: A92477; MUID:84185664; PMID:6325435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 LPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGD 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 NRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANLTFVVNSL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 LKSRKMLEEIMKYEASILTHDSSIRYLQ-----EIYNSNN-----QKIVNLKEKVAQL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 DGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETM 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 FLSSTCVA----YVATRDNCCILDERFGSYCPT-----TCGIADFLSTYQTK 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.2%; Score 480.5; DB 1; Length 437; 31.2%; Pred. No. 1e-25;
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53; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                              A;Contents: annotation; platelet aggregation region R;Dang, C:V.; Ebert, R.F.; Bell, W.R. J. Biol. Chem. 260, 9713-9719, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GDB:119132; OMIM:134850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
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A;Note: the authors translated the codon AGT for residue 105 as Åla and ATT for resid
C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F;l-24/Domain: signal sequence #status predicted <SIG>
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R; Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 6397, 1989
A; Title: Nucleotide and deduced amino acid sequence of a gamma subunit of bovine fibr A; Reference number: $05313; WUID:89366676; PMID:2771651
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Aug-1999
    al Similarity 30.6%; Pred. No. 5.9e-25;
129; Conservative 57; Mismatches 149; Indels 86; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 KYCGVPGEYWLGNDRISQLTNMGPTKLLIEMEDWKGDKVTALYEGFTVQNEANKYQLSVS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 19.4%; Score 462; DB 2; Length 444;
Best Local Similarity 30.5%; Pred. No. 2e-24;
Matches 142; Conservative 51; Mismatches 164; Indels 108; Gaps
                                                                                                                         61 LPPLTIQLPKQFSRIEE-VFKEVQNLKEIVNSLKKSCQDC--KLQADDNGDPGRNGLLLP 117
                                                                                                                                                                                                   82 LCPTGCKLQDTLVRQERPIRKSIEDLRNTVDSVSRTSSSTFQYITLLKNMWKGR----- 135
                                                                                                                                                                                                                                                                                     118 STGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKV 177
                                                                                                                                                                                                                                                                                                                                                                        136 ------QNQVQDNENVVNEYSS------HLEKHQLYIDETVKNNIPTKL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 ANLTFVVNSLDGKCSKCPSQEQIQSR------PVQHLIYKDCSDYYAIGKRSSE 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 RVLRSILENLRSKIQKLESDVSTQMEYCRTPCTVTCNIPV--VSGKECEKIIRNEGETSE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 TYRVIPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRR---- 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 MYLIQPEDSSKPYRVYCDMKTEKGGWTVIQNRODGSLDFGRKWDPYKQGFGNIATNAEGK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281 -----EFWLGNDKIHLL/TKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 NYNGTAGDAL-----RFNKHYN-HDLKFFTTPDKDNDRY----PSGNCGLYYSSGWW 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 KYKGTAGNALIEGASQLVGENRTMTIHNSMFFSTYDRDNDGWKTTDPRKQCSKEDGGGWW 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 FDACLSANLNGKYY------HQKYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIR 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 YNRCHAANPNGRYYWGGAYTWDMAKHGTDDGVVWMNWQG-----SWY--SMKKMSMKIR 462
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Best Local Similarity
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A; Residues: 1-444 <BRO>
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                                               Matches
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Arch Bacchem. Blophys. 1952, 1979
A;Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibring
A;Reference number: A37507; MUID:79164394; PMID:434821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 22-53 <MAR>
R;Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
R;Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
R;Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
N;Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen
A;Reference number: A37813; MUID:81199473; PMID:6262803
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A; Residues: 373-374 <MED>
C; Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide
C; Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide
C; Comment: Fibrinogen is a hexamer containing two sets of three nonidentical chains (alp
C; Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi
C; Keywords: blood coagulation; glycoprotein; plasma; pyroglutamic acid; sulfoprotein
F; 76-205/Domain: fibrinogen disulfide ring homology <FDR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 13-Sep-1996
Accession: A031221; B031117; B37507; A37513; S02443
R;Blomback, B.; Doolittle, R.F.
Acta Chem. Scand. 17, 1816-1819, 1963
A;Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B. A; Reference number: A03122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads A;Reference number: S02443; MUID:88211875; PMID:2966748
                              259 DGSTNFTRTWQDYKAGFGNLR------REFWLGNDKIHLLTKSKEMILRIDLEDF 307
                                                                                                                                                                                                                                                                                                                                                                                                               398 FDRDNDNRNPGDPTKHCSREDAGGWWYNRCHAANPNGRYYWGGIYTKEQADYGTDDGVVW 457
                                                                                                            278 DGSSNFARDWNTYKAEFGNIAFGNGKSICNIPGEYWLGTKTVHQLTKQHTQQVLFDMSDW 337
                                                                                                                                                                                          308 NGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDAL-----RFNKHYN-HDLKFFTT 358
                                                                                                                                                                                                                                                                    338 EGSSVYAQYASFRPENEAQGYRLWVEDYSGNAGNALLEGATQLMGDNRTMTIHNGMQFST 397
                                                                                                                                                                                                                                                                                                                                                       359 PDKDNDRY----PSGNCGLYYSSGWWFDACLSANLNGKYY-----HQKYRGVRNGIFW 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;215-464/Domain: fibrinogen beta/gamma homology <FBG>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6/Maiding site: sulfate (Tyr) (covalent) #status experimental
F;21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
F;371/E;inding site: carbohydrate (Asn) (covalent) #status predicted
F;372-373/Cleavage site: Arg-Thr (plasmin) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
FEBS Lett. 232, 56-60, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Amino acid sequence of bovine fibrinopeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.8%; Score 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               408 GTWPGVSEAHPGGYKSSFKEAKMMIRPK 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Contains: fibrinopeptide B
C;Species: Bos primigenius taurus (cattle)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 458 MNWKG----SWY--SMRQMAMKLRPK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-4 <BLO>
R; Sjoquist, J.; Blomback, B.; Wallen, P.
Ark. Kemi 16, 425-436, 1960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ibrinogen beta chain - bovine
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A; Accession: B03117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
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Riemschen, A.; Lottspeich, F.; Kell, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A; Title: Covalent structure of fibrinogen.
A; Reference number: A90037; MID: 83254370; PMID: 6575689
A; Contents: annotation; review, disulfide bonds
A; Contents: annotation; review, disulfide bonds
B; Gardlund, B.; Hessel, B.; Marguerie, G.; Murano, G.; Blomback, B.
Eur. J. Biochem. 77, 595-610, 1977
A; Title: Primary structure of human fibrinogen. Characterization of disulfide-contain
A; Reference number: A91249; MUID: 77245999; PMID: 891553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G. in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., F. A; Title: The structures of fibrinogen and fibrin.
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J. Biol. Chem. 265, 13669-13666, 1990
A;Title: A unique protocolytic fragment of human fibrinogen containing the Aalpha COOH
A;Reference number: A37117; MUID:9037977; PMID:2143188
A;Contents: annotation; hementin cleavage site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: hementin, a protease from Haementeria ghilianii, the giant South American lee C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cle ization sites responsible for the formation of the soft clot.
C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stab
                                                                                                                                                                                                                                                                      Biochemistry 33, 1988-1993, 1994
A;Title: Identification of proteins associated with apolipoprotein A-I-containing lip
A;Reference number: A54223; MUID:94162201; PMID:8117655
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A;Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR ins are contained in the core. Two three-chain coiled coils emerge from this core and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Pathway: blood coagulation
C; Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglutamic
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F;31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experi
F;44-45/Cleavage site: Arg-Gly (thrombin) #status experimental
                                                                                                                              A; Molecule type: protein
A; Residues: 31-112, E',114-137,'QS',140-144,'QF',147-148 <BLO>
R; Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 164-174 <KUN>
A;Note: identification of tryptic peptides from high-density lipoproteins
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Annu. Rev. Biochem. 53, 195-229, 1984
A;Title: Fibrinogen and fibrin.
A;Reference number: A90041; MUID:84305751; PMID:6383194
A;Contents: annotation; review, EM structure, polymerization, ligands A;Contents: annotation; review, EM structure, polymerization, ligands R;Chung, D.W.; Rixon, M.W.; Que, B.G.; Davie, E.W.

" v Acad. Sci. 408, 449-456, 1983
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A; Title: Cloning of fibrinogen genes and their cDNA.
A; Reference number: A90038; MUID:83254384; PMID:6575700
A; Reference number: A94309; MUID: 76225080; PMID: 936108
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                                                A; Contents: disulfide bonds
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                                                                                            A; Accession: A94309
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C;Sbec: 4-Apr-1994 # sequence_revision 31-Mar-1993 #text_change 08-Dec-2000
C;Accession: B43568; A90469; B90469; I37389; A94433; A90437; A94309; G54223; A03121; B37
R;Chung, D.W.; Harris, J.E.; Davie, E.W.
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A;Cross-references: GB:J00129; NID:g182429; PIDN:AAA52429.1; PID:g182430
R;Huber, P.; Dalmon, J.; Courtois, G.; Laurent, M.; Assouline, Z.; Marguerie, G. Nucleic Acids Res. 15, 1615-1625, 1997
Title: Characterization of the 5'-flanking region for the human fibrinogen beta gene.
Reference number: 137389; MUID:87146483; PMID:3029722
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Botchemistry 22, 3244-3250, 1983
A;Title: Characterization of complementary deoxyribonucleic acid and genomic deoxyribonu A;Reference number: A90469; MUID:83283433; PMID:6688356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL:X05018; NID:g31400; PIDN:CAA28674.1; PID:g31401
R; Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
h; Protides of the Biological Fluids, Proc. 28th Collog., Peeters, H., ed., pp.51-56, PA; Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural A; Reference number: A94433
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A; Title: Nucleotide sequences of the three genes coding for human fibrinogen.
A; Reference number: A43568; MUID:91344740; PMID:2102623
146 VNLRDKVVQLEANCQE-PCQDTVK---IHDVJGRDCQDVANKGAKESGLYFIRP-LKAKQ 200
                                                                                                                                                                                         292 LTKSKEM--ILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNY-NGTAGDAL---- 343
                                                                                                                                                                                                                                                                                                                                                                                                          261 ISTQSSIPYVLRIQLEDWNGRTSTADYASFKVTGENDKYRLTYAYFIGGDAGDAFDGYDF 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 ---RFNKHY-NHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYH---- 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 GDDSSDKFFTSHNGMQFSTWDSDNDKY-DGNCAEQVGIGWWMNKCHAGHLNGVYYQGGTY 379
                                                                                                                              238 FEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNL----RREFWLGNDKIHL 291
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A; Residues: 31-144, QF', 147-231, 'D', 233-330, 'E', 332-491 <WAT>
R: Blomback, B:, Hessel, B:, Hogg, D.
Thromb. Res. 8, 639-658, 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 SKTSTPNGYDNGIIWATW------KSRWYSMKKTTMKIIP 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 --- QKYRGVRNGIFWGTWPGVSEAHPGGYKS---SFKEAKMMIRP 434
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A;Residuses: 31-137, OS.',140-144,'QF',147-491 <HEN>
Matt, K.W.K.; Takagi, T.; Doolittle, R.F.
Biochemistry 18, 68-76, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N; Alternate names: coagulation factor I
N; Contains: fibrinopeptide B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 9-191,'P',193-491 <CHU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Contents: carbohydrate binding
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A; Residues: 1-38 <CH1>
A; Accession: B90469
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A; Residues: 1-38 <HUB>
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ficolin-A precursor - mouse (;Species: Mus musculus (house mouse) (c)Species: Mus musculus (house mouse) (c)Date: 06-May-1998 #sequence_revision 29-May-1998 #text_change 18-Feb-2000 (c)Accession: JG5980 (f) The more of the mouse of the mou
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A; CCOSS-references: DDBJ:AB007813; NID:g2957011; PIDN:BAA25126.1; PID:d1026054; PID:g
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                        70; Gaps
                                                                                                                                                                                                                                                                                                 70 KQFSRIEE-VFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN 128
                                                                                                                                                                                                                                                                                                                                                                                          51 DFLNRYQENVDTDLQYLENLLTQISNSTSGTTIIVEHLIDSGKKPATSPQTAI-----DP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 RVRELESEVNKLSSELKNAKE-EINVLHGRLEKLNLVNMNNIENYVDSKVANLTFVVNSL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 MTQKSKTCWMKL-TDMKNYYQYEBNILY--LQEVYSSNQNKI-FLLKQKIANLEL---- 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 DGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETM 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 -- QCQQ-PCRDTVQ---IQEFTGKDCQEVANKGARLSGLYYIKPLKAKQQFLVYCETEPS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 GGGWTVLQARLDGSTNFTRTWQDYKAGFG----NLRREFWLGNDKIHLLTKSKEM--ILR 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 GSAWTVIQRRLDGSVNFHKNWVQYREGFGYLSPNDKTEFWLGNEKIHLLSTQSTIPYVWR 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 IDLEDFNGVELYALYDQFYVANEFLKYRLHVGNY-NGTAGDAL------RFNKHY-NH 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 IELEDWSNOKSTADYSTFRLGSEKDNYRFTYAYFIGGDAGDAFDGFDFGDDPSDKFYTSH 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352 DLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYH------QKYRGVRN 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 NGMQFSTFDKDNDKF-DGNCAEQDGSGWWMNRCHAAHLNGKYYQGGTYSEADSGPSGYDN 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 LGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNY-NGTAGDA 342
                                                                                                             10 SSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVSLPPLTIQLP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 GDPGRNGLLLP--STGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 GSPGKMG---PAGSKGEPGTMGPPGVKGEKGDTGAAPS---LGEKELG------ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 NANNIENYVDSKVANLTFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --DTLCQRGP-----RSCKDLLTRGIFLT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 ETYRV-TPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFW 283
                                                                                                                                                                                                  14 SLALLSSAFGNIIPNTDNCCILDGRFGEYCPT-----TCGIS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 334;
                   Matches 130; Conservative 69; Mismatches 158; Indels
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F;1-21/Domain: signal sequence #stetus predicted <SIG>
F;0-64,68-106/Domain: collagen-like #status predicted <COL>
F;123-334/Domain: fibrinogen beta/gamma homology <FBG>
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Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404 GIFWGTW 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390 GIIWATW 396
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R;Bhattacharya, A.; Shepard, A.R.; Moser, D.R.; Holland, L.J.
Mol. Cell. Endocrinol. 72, 213-220, 1990
A;Title: Isolation and characterization of cDNA clones for the gamma subunit of Xenopus A;Reference number: I51416; MUID:91146806; PMID:2289632
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A;Ittle: Estrogen regulation of Kenopus laevis gamma-fibrinogen gene expression. A;Reference number: A32670; MUID:90241882; PMID:2334684
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C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 13-Aug-1999
:Accession: A32670; 151416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 TQKKVERKAPDA-----GGCLHADPDLGVLCPTGCQLQEALLQQERPIRNSVDELNN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 EVQNLKEIVNS-----LKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVREL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 NVEAVSQTSSSSFQYMYLLKDLWQKRQKQVKDN------------------------165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 ESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANLTFVVNSLDGKCSK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 CPSQEQIQ-----SRPVQHLIYKDCSDYYALGKRSSETYRVTPDPKNSSFEVYCD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 ENVVNEYSSE------LEKHQLYIDETVNSNIPTNLRVLRSILENLRSKIOK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 LESDVSAQMEYCRTPCTVSCNIPVVSGKECEEIIRKGGETSEMYLIQPDSSVKPYRVYCD 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 METMGGGWTVLQARLDGSTNFTRTWQDYKAGFGN------LRREFWLGNDKIHL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272 MNTENGGWTVIQNRQDGSVDFGRKWDPYKQGFGNVATNTDGKNYCGLPGEYWLGNDKISQ 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 LTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALR----- 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 LTRMGPTELLIEMEDWKGDKVKAHYGGFTVQNEANKYQISVNKYRGTAGNALMDGASQLM 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 -FNKHYN-HDLKFFTTPDKDNDRY----PSGNCGLYYSSGWWFDACLSANLNGKYY---- 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 TEEIKDERAKDVCPVRLESRGKCEEAGE-----CPYQVSLPPLTIQLPKQF-SRIEEVFK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 GENRTMIIHNGMFFSTYDRDNDGWLJSDPRKQCSKEDGGGWWYNRCHAANPNGRYYWGGQ 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M35548; NID:g214141; PIDN:AAA03247.1; PID:g214142 CS:Superfamilly: fibrinogen gamma chain; fibrinogen beta/gamma homology C;Keywords: blood coagulation C;Keywords: blood coagulation F:173-413/Domain: fibrinogen beta/gamma homology <FBG>
                                                                                                                                                                                        F;394/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:110/Disulfide bonds: interchain (to gamma-45) #status experimental F:223/Disulfide bonds: interchain (to alpha-184) #status experimental F:227/Disulfide bonds: interchain (to gamma-161) #status experimental F:231-316,241-270,424-437/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                     161; Indels 112;
                                                                                                                                                                                                                                                                                  19.4%; Score 461; DB 1; Length 491; 28.7%; Pred. No. 2.6e-24; Live 57; Mismatches 161; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 19.2%; Score 456; DB 2; Length 438; Best Local Similarity 30.4%; Pred. No. 5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  395 ---HQKYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRP 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452 YTWDMAKHGTDDGVVWMNWKG----SWY--SMRKMSMKIRP 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fibrinogen gamma chain - African clawed frog
                                                                                                                                                                                                                                                                                                                                                                           Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-438 <PAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-58 <BHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A32670
                                                                                                                                                                                                                                                                                  Query Match
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F;461-491/Disulfide bonds: #status experimental
F;527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #stat
F;686,831/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fibrinogen related protein A precursor - sea cucumber (Parastichopus parvimensis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Parastichopus parvimensis
C;Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 09-Sep-1997
C;Accession: A35084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence in an echinoderm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 YLLVLGAYSGTAGDSLAY----HNTMRFSTYDNDNDVY-SINCASHSSYGRGAWWYKSC 240
                                                                                                                                                                                                                                                                                                                                                                                                                   476 KEV--TKEVVTS--EDGSDCP-EAMDLGTLSGIGTLDGFRHRHPDEAAFFDTASTGKTFP 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 STGAP--GEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLE---------KLN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                531 GFFSPMLGEF----VSETESRGSE-SGIFTNTKESSSHHPGIAEFPSRGKSSSYSKQFTS 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 LVNMNNIENYVDSKVANLTEVVNS-LDGKCSKCPSQEQIQSRPVQHLIYKDCSDY---YA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            586 STSYNRGDSTFESKSYKMADEAGSEADHEGTHSTKRGHAKSRPV-----RDCDDVLQTHP 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 IGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 ----RREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGN 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               700 NDEGEGEFWLGNDYLHLLTQ-RGSVLRVELEDWAGNEAYAEY-HFRVGSEAEGYALQVSS 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 YNGTAGDAL-----RENKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                758 YEGTAGDALIEGSVEEGAEYTSHNNMQ ---FSTFDRDADQWEE-NCAEVYGGGWWYNNCQ 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75; Indels 22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 KDCSDYY--AIGKR-SSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 RDCYDILQSCSGQSPPSGQYYIQPDGGN-LIKVYCDMETDEGGWTVFQRRIDGTINFYRS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 WQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 YRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSGG---WWFDAC 384
                                                                                                                                                                                                                                                                                                                                  -----DPGRNGLLLP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     386 SANLNGKYY------HQKYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRP 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 282;
                                                                                                                                                                     Length 866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 LSANLNGKYYHQKYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIR 433
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Silver. 87, 2097-2101, 1990
A;Tille Presence of a vertebrate fibrinogen-like sequen
A;Reference number: A35084; MUID:90192754; PMID:2315305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB: M31326; NID: 9161164; PID: 9161165
                                                                                                                                                                                                ; Pred. No. 2.8e-23; 51; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;67-280/Domain: fibrinogen beta/gamma homology <FBG>
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                                                                                                                                                                     19.0%; Score 451; DB 2;
                                                                                                                                                                                                                                                                                                                                  80 KEVQNLKEIVNSLKKSCQDCKLQADDNG-----
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                                                                                                                                                                                                              32.5%;
                                                                                                                                                                                                                                                      Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Xu, X.; Doolittle, R.F.
                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-282 <XUX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary A; Molecule type: mRNA
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                                                                                                                                                                              Query Match
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C; Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibronectin.
C; Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave ization sites responsible for the formation of the soft clot.
C; Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili ger) and between alpha chains (weaker) of different monomers.
C; Comment: All fibrinogen chains are synthesized in the liver.
C; Comment: See PIR:FGHUA for the major splice form. It is not known whether this form is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F:288,419/Binding site: carbohydrate (Asn) (covalent) #status absent
F:322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #
F:347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp
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A;Introns: 18/3; 60/3; 122/1; 171/2
A;Note: the list of introns is incomplete
C;Complex: The fibrinogen molecule is a hexamer containing two sets of three nonidentica
tained in the core. Two three-chain coiled coils emerge from this core and connect it t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Homo sapiens (man)
Space: Homo sapiens (man)
Space: 10-Jun-1993 # sequence_revision 06-Sep-1996 #text_change 19-Jan-2001
Spaces: 10-Jun-1993 # sequence_revision 06-Sep-1996 #text_change 19-Jan-2001
Fur Y: Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redma Dchemistry 31, 11968-11972, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M58569; NID:9182406; PID:9182407
A;Note: neither the complete nucleic acid sequence nor the complete translation are show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a nove A;Reference number: A44234; MUID:93090725; PMID:1457396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into A; Pathway: blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: human extended splice form fibrinogen alpha chain; fibrinogen beta/gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-863/Product: fibrinopen alpha chain, extended splice form #status predicted <MAT>
F;30-35/Product: fibrinopeptide A #status experimental <APT>
F;36-863/Product: fibrin alpha chain, extended splice form #status predicted <FGA>
F;57-185/Domain: fibrinogen disulfide ring homology <FDR>
        343 LRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR 402
                                                                                                                                                                                                              256 L--TKHNNMS---FTTHDQDNDA-NSMNCAALFHGAWWYHNCHQSNLNGRYLSGSHESYA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;22,460/Binding site: phosphate (Ser) (covalent) #status experimental F;35-36/Cleavage site: Arg-Gly (thrombin) #status experimental F;47/Disulfide bonds: interchain (to alpha-47) #status experimental F;55/Disulfide bonds: interchain (to beta-95) #status experimental F;64/Disulfide bonds: interchain (to gamma-49) #status experimental F;68/Disulfide bonds: interchain (to beta-106) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;180/Disulfide bonds: interchain (to gamma-165) #status experimental F;184/Disulfide bonds: interchain (to beta-223) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fibrinogen alpha chain precursor, extended splice form - human N;Alternate names: coagulation factor I N;Contains: fibrinopeptide A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;591-593/Region: cell attachment (R-G-D) motif
F;629-863/Domain: fibrinogen beta/gamma homology <FBG>
                                                                                                                                                                                                                                                                                                   403 NGIFWGTWPGVSEAHPGGYKSSFKEAKMMIR 433
                                                                                                                                                                                                                                                                                                                                                                               310 DGINWGTGQ-----GHHYSYKVAEMKIR 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GDB:119129; OMIM:134820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA; DNA A; Residues: 1-866 <FUl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA; DNA A; Residues: 605-866 <FU2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tal domain nodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: D44234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: B44234
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Db 241 LLSNLNGQYY--DYSGAPS-IYWSYLPGDNDQIP-----FAEMKLRNR 280

Search completed: December 2, 2002, 06:54:01 Job time : 32.9427 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

December 2, 2002, 06:41:25; Search time 36.7445 Seconds Run on:

(without alignments)
495.533 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-902-563-2 2378 1 MKLANWYWLSSAVLATYGFL......GYKSSFKEAKMMIRPKHFKP 439

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched: tal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	14314 homo sapie	mus m	035608 mus musculu	077802 bos taurus		gallu	homo) home	mus m	P02679 homo sapien	mus m	Q9uku9 homo sapien		P02676 bos taurus	Q9wvh6 mus musculu	018920 bos taurus	P12799 bos taurus	P02675 homo sapien	P17634 xenopus lae	rat	mus n	homo	Q9y264 homo sapien	paras	~	m	P04115 petromyzon	6 rattus		hom 2	7	485	P02680 rattus norv
SUMMARIES,	ID	GL2_H	FGL2_MOUSE	AGP2_MOUSE	AGP2_BOVIN	AGP2_HUMAN	FIBB_CHICK	FGL1_HUMAN	AGP1_HUMAN	ANL2_MOUSE	FIBG_HUMAN	AGP1_MOUSE	ANL2_HUMAN	FIBB_PETMA	FIBB_BOVIN	AGP4_MOUSE	AGP1_BOVIN	FIBG_BOVIN	FIBB_HUMAN	FIBG_XENLA	FIBB_RAT	FCN1_MOUSE	FIBA_HUMAN	AGP4_HUMAN	FIBA_PARPA	FIBA_RAT	FCN1_RAT	FIBG_PETMA	FCN2_RAT	FIBA_CHICK	FCN1_HUMAN	FCN2_MOUSE	FCN2_HUMAN	FIBG_RAT
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	Length	439	432	496	375	496	463	312	498	493	453	498	493	477	468	509	481	444	491	438	479	334	998	503	282	782	335	432	319	741	326	306	313	445
d	Query Match	0.00	77.9	22.1				21.3		20.4								19.4				19.0				18.5	18.4	18.0	œ.	ω.		17.7		17.6
	Score	237	1853.5	525	524.5	522	511.5	506.5	486.5	485.5	84	483.5	480.5	479.5		470.5	467	462	461	456	454.5	452	451	450	446	441	438.5	428.5	428	427.5	427	421.5	7	419
	Result No.		2	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

075636 homo sapien P55083 homo sapien P22105 homo sapien P24821 homo sapien 029116 sus scrofa P10039 gallus gall P33573 petromyzon P21520 drosophila 03562 rattus norv P55918 bos taurus Q58718 methanococc P25805 plasmodium
FCN3_HUMAN MFA4_HUMAN TENX_HUMAN TENA_HUMAN TENA_CHICK FIRA_PETMA SCA_DROME ASP2_RAT MFA4_BOVIN RA50_METJA CYSP_PLAFA
299 255 4289 2201 1746 1808 641 774 137 129 1005
106.3 116.2 116.2 11.9 11.9 11.9 11.9
414.5 399.397.5 388.388.5 386.5 386.5 346.5 116.5
888888844444486000000000000000000000000

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                   61 LPPLTIQLFKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG 120
                                                                                                                                                                                                                                                                                                                                                       61 LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG 120
                                                                                                                                                                                                                                                                                                                                            121 APGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANL 180
                                                                                                                                                                                                                                                                                                                                                                                                                 241 YCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMIL 300
                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 KDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVRNGIFWGTWPGVSEAHPGG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLANWYWLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVS 60
                                                                                                                                                                                                                                                                               01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
115-0CT-2001 (Rel. 40, Last annotation update)
Fibroleukin precursor (Fibrinogen-like protein 2) (Prothrombinase)
FGLOOM FIBLP.
                                                                                                                                                    N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                      DB 1; Length 439;
                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                  DF34656288E49E68 CRC64;
                                                                                                                            FIBRINOGEN C-TERMINAL.
                                                                                                                                                                                                                           Score 2378; DB 1, No. 2.8e-153;
                                                                                                                                                                                                          FTIG=VAR_013066
                                                               Interrio; trucco...
SMART; SMO1147; fibrinogen_C; 1.
SMART; SMO1166; FBG; 1.
PROSITE; PSO0514; FIBRIN_AC_DOMAIN; 1.
T-cell; Glycoprotein; Signal; Polymorphism.
23
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                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                     BY SIMILARITY
                                                                                                                                              BY SIMILARITY
                                                                                                                   FIBROLEUKIN.
       EMBL; AF104015; AAD10825.1; -. EMBL; AF104014; AAD10825.1; JOINED. EMBL; AF468959; AAL68855.1; -.
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                                                            IPR002181; Fibrinogen_C.
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                                                                                                                                                                                                                 439 AA; 50228 MW;
                                                                                                                                                                                                                                    100.08;
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EMBL; Z36531; CAA85298.1;
                                                                                                                                                                                                                                           Local Similarity 100.0
nes 439; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                            HGNC:3696; FGL2.
                                                                                                                          2435
384
384
179
235
336
                                  HSSP; P02671; 1FZD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGL2_MOUSE
P12804;
                                                    MIM; 605351
                                                              InterPro:
                                                                                                                                   DISULFID
                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                        CARBOHYD
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                                                                                                                                                                                                 VARIANT
                                             Genew;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLANWYWLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRLPGWLWLSSAVLAACR-AVEEHNLTEGLEDASAQAACPARLEGSGRC-EGSQCPFQLT 58
                                                                                                                                                                                                                                        Koyama T., Hall L.R., Haser W.G., Tonegawa S., Saito H.;
"Structure of a cytotoxic T-lymphocyte-specific gene shows a strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Association of mouse fibrinogen-like protein with murine hepatitis
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- INDUCTION: IN MACROPHAGES, DURING INFECTION BY MOUSE HEPATITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parr R.L., Fung L., Reneker J., Myers-Mason N., Leibowitz J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.9%; Score 1853.5; DB 1; Length 432; 77.7%; Pred. No. 6.3e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- FUNCTION: CONVERTS PROTHFOMBIN TO THROMBIN.
-1- SUBUNIT: HOMOTETRAMER, DISULFIDE-LINKED (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIRUS STRAIN 3 (MHV-3).
-!- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A -> G (IN REF. 2).
2B297F69CCB4A782 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIBRINGEN C-TERMINAL.
                                                                                                                                                                                                                                                                                              homology to fibrinogen beta and gamma chains."; Proc. Natl. Acad. Sci. U.S.A. 84:1609-1613(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BALB/CJ; TISSUE-Peritoneal macrophage;
MEDLINE-95333285; PubMed-7609073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Mismatches
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIBROLEUKIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virus-induced prothrombinase activity."
J. Virol. 69:5033-5038(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002181; Fibrinogen_C. Pfam; PF00147; fibrinogen_C; 1.
                                                                                                                                                                               TISSUE=Cytotoxic T-cell;
MEDLINE=87175527; PubMed=3550794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M16238; AAA37624.1; -.
EMBL; M15761; AAA37624.1; JOINED.
EMBL; S78773; AAB34823.1; -.
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MGD; MGI:103266; F912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00186; FBG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A27447; A27447.
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH AS VEGF, ANGZ-MEDIATED LOCSENING OF CELL-MARTX CONTACTS MAY INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR REGRESSION. IN CONCEPT WITH VEGF, IT MAY FACILITARIE ENDOTHELIAL CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
                                                                                                                                                                                                                                                                                   354 RDNDRYPSGNGGLYYSSGWWPDSCLSANLNGKYYHQKYKGVRNGIFWGTWPGINQAQPGG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION BINDS TO THEZ RECEPTOR AND COUNTERACTS BLOOD VESSEL MATURATION/STABILLTY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
121 APGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANL 180
                           181 TEVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEV 240
                                                                                                           301 RIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPD 360
                                                                                                                                                                                                                                                                                                                                             361 KDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVRNGIFWGTWPGVSEAHPGG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Uterus;
MEDILNE-97349377; Pubmed-9204896;
Maisonpierre P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J.,
Raditejewski C., Compton D.L., McClain J., Aldrich T.H.,
Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
"Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
                                                                                                                                                                       241 YCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMIL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: EXPRESSED ONLY AT SITES OF VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Angiopoietin-2 precursor (ANG-2).
ANGPT2 OR AGPT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF004326; AAB63189.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                   421 YKSSFKEAKMMIRPKHFKP 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 YKSSFKQAKMMIRPKNFKP 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:1202890; Agpt2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 277:55-60(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANGIOGENIC SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGP2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
AGP2_MOUSE
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                                                                                                                                                                                                                                                              δλ
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                                                                                                                                                                                                                                                                                                                                                  δy
                                                                                        δ
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121 APGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRL-----EKLNLVNMNNIENY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 LQKQQHDLMETVNSLLITMMSSPNSKSSVAIRKEEQTTFRDCAEIFKSGLTTSGIYTLTFP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 PKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293 TKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHD 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 LKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWP 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423 ---FSTKDSDNDKCIC-KCSQMLSGGWWFDACGPSNLNGQYYPQKQNTNKFNGIKWYWK 478
                                                                                                                                                                                                                                                                                                                                               61 LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG 120
                                                                                                                                                                                                                                                                                                                                                                     192 -----EQKVLDMEGKHSEQLQSMKEQKDELQVLVSKQSSVIDELEKKLVTATVNN--5L 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 VDSKVANLTFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPD 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Ovary;
MEDLINE-99054348; PubMed-9840613;
Goede V., Schmidt T., Kimmina S., Kozian D., Augustin H.G.;
"Analysis of blood vessel maturation processes during cyclic ovarian
                                                                                                                                                                                                                                                                                                               40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelegstomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                             N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                               22.1%; Score 525; DB 1; Length 496; 32.9%; Pred. No. 2.7e-28;
                                                                                                                                                                                                                                                                                                               65; Mismatches 154; Indels
                                                                                                                                                                                                                                              FA3021FE4E01C410 CRC64;
                                                                                                             COILED COIL (POTENTIAL). FIBRINGEN C-TERMINAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 077802; 0975K0;
16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
                                                                                               ANGIOPOIETIN-2.
                                              PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1. Glycoprotein; Coiled coil; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 GVSEAHPGGYKSSFKEAKMMIRPKHF 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  479 G----SGY--SLKATTMMIRPADF 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Angiopoletin-2 (ANG-2) (Fragment).
InterPro; IPR002181; Fibrinogen_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lab. Invest. 78:1385-1394(1998).
                                                                                                                                                                                                                                                  56616 MW;
              Pfam; PF00147; fibrinogen_C; SMART; SM0186; FBG; 1.
                                                                                                                                                                                                                                                                                                                 Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
                                                                                                                                                                                                                                                496 AA;
                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      angiogenesis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANGPT2 OR ANG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGP2_BOVIN
                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                   CARBOHYD
                                                                                                                  DOMAIN
                                                                                                                                   DOMAIN
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                                                                                                    CHAIN
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COILED COIL (POTENTIAL).
                                                                   401 VR-NGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANGIOPOIETIN-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 2).
TISSUE-Umbilical vein endothelial cells;
MEDLINE-20309815; Pubmed-10766762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human angiopoietin-2.";
J. Biol. Chem. 275:18550-18556(2000).
                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002181; Fibrinogen_C. Pfam; PF00147; fibrinogen_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97349327; PubMed=9204896;
                                                                                                                                                                                                                                                                                                        Angiopoietin-2 precursor (ANG-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF187858; AAF76526.1; -.
                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 277:55-60(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:485; ANGPT2.
                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00186; FBG; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANGIOGENIC SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                            015123; Q9NRR7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 601922;
                                                                                                                                                                                                           AGP2_HUMAN
                                                                                                                                                                     RESULT 5
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                                                                   οy
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                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: Secreted.
-1- DEVELOPMENTAL STAGE: FOUND TO BE EXPRESSED THROUGHOUT THE OVARIAN CYCLE. OVEREXPRESSED DURING LUTBOLYSIS, THIS COULD REFLECT THE REGRESSION OF CAPILLARIES THAT HAD DEVELOPED PERICYTE CONTACT IN THE MIDSTAGE CORPUS LUTBUM.
                                                                                                                                                          MATURATION/STABILLITY MEDIATED BY ANGIOPOLETIN'1. ITS FUNCTION MAY BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.2%; Pred. No. 2.1e-20,
tive 58; Mismatches 139; Indels 65; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LPPLTIQLPKQFSRIEEVFKEVQNLKEIV -- NSLKKSCQD-----CKLQADDNGDPGRNG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 LLLPSTGAPGEVGDNRVRELESEVNKL,SSELKNAKEEINVLHGR-----LEK-LNLVN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 FL-----EKKVLDMEDKHIVQLRSIKEEKDQLQVLVSKQNSIIEELEKQLVTAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 MNNI----ENYVDSKVANLTFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 VNNSVLOKQOHDLMETVNNLLTLMSTSNPSYSLLAKDEQI-----IFRDCGEAFKSG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 KRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRR 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281 EFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 EHWLGNEFVSOVTGOKRYVLKIHLRDWEGNEAYSLYDHFYLSNEELNYRIHLKGLTGTAG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 DALRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 LIDVEAQVLNGTTRL----ELQLLEHSLSTNKLEKQILDQTSEISKLQ------DKNS 69
                                                       Mandriota S.J., Pepper M.S.;
"Regulation of angiopoietin-2 mRNA levels in bovine microvascular endothelial cells by cytokines and hypoxia.";
Circ. Res. 83:822-859(1998).
-i- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
S -> L (IN REF. 2).
6F086C4A5C80050A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 375;
                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIBRINGEN C-TERMINAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.1%; Score 524.5; DB 1 34.2%; Pred. No. 2.1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1. Glycoprotein; Coiled coil.
                                                                                                                                                        MATURATION/STABILITY MEDIATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR002181; Fibrinogen_C.
                                      MEDLINE=98451564; PubMed=9776732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF094699; AAC62490.1; -.
SEQUENCE OF 219-355 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF032924; AAC78285.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375 AA; 42761 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00147; fibrinogen_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                   TISSUE-Adrenal cortex;
                                                                                                                                                                                                                                                                             ANGIOGENIC SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00186; FBG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
183
272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE CONTEXT DEPENDENT. IN THE ABSENCE OF ANGIGGENIC INDUCERS, SUCH AS VEGF, ANG2-MEDIATED LOGSENING OF CELL-MATRIX CONTACTS MAY INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITS FUNCTION MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malsonpierre P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J., Radžiejewski C., Compton D., McClain J., Aldrich T.H., Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.; "Anglopoietin-2, a natural antagonist for Tiez that disrupts in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim I., Kim J.-H., Ryu Y.S., Jung S.H., Nah J.J., Koh G.Y.; "Characterization and expression of a novel alternatively spliced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: BINDS TO TIEZ RECEPTOR AND COUNTERACTS BLOOD VESSEL MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
-1- SIMILARITY: CONTAINS 1 FIBRINGGEN C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
Glycoprotein; Coiled coil; Signal; Alternative splicing.
SIGNAL 1 16 POTENTIAL.
346 NKFNGIKWYYWKG----SGY--SLKATTMMIRPADF 375
                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                        496 AA.
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15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDN 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 LKDWEGNEAYSLYEHFYLSSEELNYRIHLKGLTGTAGKISSISQPGND----FSTKDGDN 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431 DKCIC-KCSQMLTGGWWFDACGPSNLNGMYYPQRQNTNKFNGIKWYYWKG-----SGY- 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                               85 LKE-----IVNSLKKSCODCKLOADDNGDPGRNGLLLPSTGAPGEVGDN---- 128
                                                                                                                                                                                                                                                                                                                                                                                                                          129 -----RVRELESEV-----LEKL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 TAEQTRKLTDVEAQVLNQTTRLELQLLEHSLSTNKLEKQILDQTSEINKLQDKNSFLEKK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 NLV-------V 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 VLAMEDKHIIQLQSIKEEKDQLQVLVSKQNSIIEELEKKIVTATVNNSVLQKQQHDLMET 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 VNNLLTMMSTSNSAKDPTVAKEEQISFRDCAEVFKSGHTTNGIYTLTFPNSTEEIKAYCD 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 METMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRID 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315 MEAGGGGWTIIQRREDGSVDFQRTWKEYKVGFGNPSGEYWLGNEFVSQLTNQQRYVLKIH 374
                                                                                                                                                                                                                                                                                                                                                                                  86 IMENNTQWLMKLENYIQDNMKKEMVEIQQNAVQN------QTAVMIEIGTNLLNQ 134
                                                                                                                                                                                                                                 74; Mismatches 159; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                          26 MDSIGKKOYQVQHGSCSYTFLLPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLEN 85
                                                                                                                                                                                                                                                                       43 LESRGKCE---EAGECPYQVSLPPL------TIQ--LPKQFSRIEEVFKEVQN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weissbach L., Oddoux C., Procyk R., Grieninger G.; "The beta chain of chicken fibrinogen contains an atypical thrombin
                  N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B]
                                                                                                                                                                                            DB 1; Length 496;
                                                                                                                                                     5642A58847A7385C CRC64;
  FIBRINGEN C-TERMINAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
                                                                                                                                  MISSING (IN ISOFORM 2
                                                                                                                                                                                                               Pred. No. 4.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463 AA.
                                                                                                                                                                                            Score 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91182745; PubMed=2009266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochemistry 30:3290-3294(1991).
                                                                                                                                                       56919 MW;
                                                                                                                                                                                          22.0%;
                                                                                                                                                                                                               27.98;
                                                                                                                                                                                                                               Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423 SSFKEAKMMIRPKHF 437
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1133
1151
2240
304
148
                                                                                                                                                                                                               Local Similarity
                                                                                                                                                       496 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIBB_CHICK
Q02020;
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                                                            CARBOHYD
                                                                                                                                                       SEQUENCE
                    CARBOHYD
                                                                                                 CARBOHYD
                                                                                                                    CARBOHYD
                                                                                                                                                                                              Query Match
                                       CARBOHYD
                                                                                                                                    VARSPLIC
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                   the Swiss Institute of Bioinformatics and the EMBL outstation
-!- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                 MISCELLANBOUS: CONVERSION OF FIGURATIONS AND B FROM ALPHA & BETA THROMBIN, WHICH CLEAVES THEN INDEPTIDES A AND B FROM ALPHA & BETA PRINTS, AND THUS EXPOSES THE N-FERMINAL POLYMERIZATION SITES PREPONSITAL FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
                                                                                                                                                                                                               EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
INTERCHAIN (WITH GAMAR) (BY SIMILARITY).
INTERCHAIN (WITH GAMAR) (BY SIMILARITY).
INTERCHAIN (WITH GAMARA) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 137; Conservative 71; Mismatches 154; Indels 89; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 ODKOAMKKGPIIYPDAGGCKHPLDELGVLCPTGCE---LQTTLLKQEKTVKPVLRDLKDR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 -----LKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVRELE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 VAKFSDTSTTMYQYVNMIDNKLVKTQKQRKD-----NDIILSEYNTEMELHYNYIK--D 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 SEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANLTFVVNSLDGKCSKC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 NLDNNIPSSLRVLRAVIDSLHKKIQKL-----ENAIATQT-----DYCRSPC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 PSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 -----VASCNIPVVSGRECEDIYRKGGETSEMYIIQPDPFTTPYRVYCDMETDNGGWTLI 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 QARLDGSTNFTRTWQDYKAGFGNLRR------EFWLGNDKIHLLTKSKEMILRID 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 ONRODGSVNFGRAWDEYKRGFGNIAKSGGKKYCDTPGEYWLGNDKISOLTKIGPTKVLIE 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALR--FNKHYN------HDLK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
                                                             -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS
                                                                                                                                                                       RESPONSTBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XIIIA WHICH CATALYZES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 KDERAKDVCPVRLESRGKC----EEAGE-CPYQVSLPPLTIQLPKQFSRIEEVFKEVQN- 84
                                                                                                          MISCELLANEOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. .) (POTENTIAL). 2044CD49BA79EC7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 463;
                                                                                                                                                                                                                                         (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIBRINOGEN BETA CHAIN.
SULFATION (BY SIMILARITY).
CLEAVAGE (BY THROMBIN; RELEASE
                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 FIBRINGEN C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIBRINOPEPTIDE B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIBRINOPEPTIDE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.5%; Score 511.5; DE 30.4%; Pred. No. 2e-27;
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P02675; IFZF.
InterPro; IPR002181; Fibrinogen_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00147; fibrinogen_C; 1.
SMART; SM00186; FBG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52678 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M58514; AAA48770.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A38463; A38463.
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397
367
463 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                            AGGREGATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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355 FFTTPDKDNDRY----PSGNCGLYYSSGWWFDACLSANLNGKYY-----HQKYRGVRN 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human hepassocin, a liver-specific protein with hepatocyte mitogenic
                                                                                                                                                                                          008830; 0960M6; 096KW6;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fibrinogen-like protein 1 precursor (Hepatocyte-derived fibrinogen-related protein 1) (HFREP-1) (Hepassocin) (HP-041).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21363035; PubMed-11470158;
Hara H., Yoshimura H., Uchida S., Toyoda Y., Aoki M., Sakai Y.,
Morimoto S., Shiokawa K.;
"Molecular cloning and functional expression analysis of a cDNA for
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular cloning and initial characterization of a novel
                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto T., Gotoh M., Sasaki H., Terada M., Kitajima M.,
Hirohashi S.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- TISSUE SPECIFICITY: Liver-specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                 fibrinogen-related gene, HFREP-1.";
Biochem. Biophys. Res. Commun. 193:681-687(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --- FUNCTION: Has hepatocyte mitogenic activity.
--- SUBUNIT: Homodimer (Probable).
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Liver-specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                       404 GIFWGTWPGVSEAHPGGYKSSFKEAKMMIRP 434
                                                                                                                437 GIVWMNWKG-----SWY--SMKKMSMKIKP 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochim. Biophys. Acta 1520:45-53(2001).
                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE #93290661; PubMed = 8390249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002181; Fibrinogen_C. Pfam; PF00147; fibrinogen_C; 1. SMART; SM00186; FBG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC007047; AAH07047.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D14446; BAA03336.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAB70690.1; -.
                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:3695; FGL1.
                                                                                                                                                                                                                                                                                       sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D87342;
                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver
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Gaps 10;
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Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
Ryan T.E., Bruno J., Radziejewski C., Malsonpierre P.C.,
                                                                                                                                                                                                                                                                                                                                                                                                 131 RELESEVNKLSSELKNAKEEINVLHGRLE----KLNLVNMNNIENYVDSKVANLTFVVNS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 -GGGWTVIQRRSDGSENFNRGWRDYENGFGNFVQKHGEWLGNKNLHFLFTQEDYTLKID 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 LDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMET 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 ------SKRQ-------YADCSEIFNDGYKLSGFYKIKPLQSPAEFSVYCDMSD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 MGGGWTVLQARLDGSTNFTRTWQDYKAGFGNL---RREFWLGNDKIHLLTKSKEMILRID 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 TPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRG-VRNGIFWGTWPGVSEA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKH-----YNHDLKFFT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                          18 REI-SALEDCAQEQMRLRAQVRLLETRVKQQQVKIKQLLQENEVQFLDKGDENTVIDLG- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by secretion-trap expression cloning.";
                                                                                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                                                                 DB 1; Length 312;
                                                                                                                                                                                                                                                                                                          21.3%; Score 506.5; DB 1; Length 36.8%; Pred. No. 2.7e-27; tive 40; Mismatches 119; Indels
                                                                                                                                                                          I -> T (IN REF. 3).
N -> D (IN REF. 1).
I -> V (IN REF. 1).
P -> L (IN REF. 2).
A; 26BC82124E6660C2 CRC64;
                                                                    FIBRINGEN-LIKE PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohara O., Nagase T., Kikuno R., Nomura N.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                               INTERCHAIN (POTENTIAL).
                                                                                         FIBRINOGEN C-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               498 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANT GLY-269 DEL
                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417 HPGGYKSSFKEAKMMIRPKHFKP 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 -- HGWWYSLKSVVMKIRPNDFIP 309
                                     23 32
78 305
78 305
26 26
3 112
9 261
169
72 1
105
36391 MW,
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                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                    312 AA;
                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Bone marrow;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Q15389;
                                                                                                                                                                                                                                                                                                                                                       119;
                                                                                                                                                                                                                  CONFLICT
CONFLICT
SEQUENCE
                                                                                                            DISULFID
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                                                                                                                                  DISULFID
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                                                                                                                                                       DISULFID
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                            Signal.
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P02671; 1FZD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                    ANGPTL2 OR ARP2
                                                                                                                                                                                                                                                                                      ANL2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sprouting.
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                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . ) (POTENTIAL).
MISSING (IN CELL LINE T98G; MAY BE DUE TO
                                                                                                                                                                                                                                                              -!- MISCELLANDOUS: IT MAY HAVE A POTENTIAL THERAPBUTIC UTILITY SINCE IT CAN BE USED FOR SPECIFICALLY TARGETING TUMOR VASCULATURE OR FOR
                                                                                                     DNA RES. 1:27-35(1994).

-!- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPERRS TO PLAY A CRICIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE HEART EARLY DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LPPLTIQLPKQFSRIE------EVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 NLVNMNNIENYVDSKVANLTFVVNSLDGKCSK----CPSQEQIQSRPVQHLIYKDCSDYY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 AIGKRSSETYRV----TPDDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 LTDVETQVLNQTSRLEIQLLENSLSTYKLEKQLLQQTNEILKIHE------KN 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 GLLLPSTGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHG------RLEK-L 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 SLL------EHKILEME---GKHKEELDTLKEEKENLQGLVTRQTYIIQELEKQL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 NRATTNN--SVLQKQQLELMDTVHNLVNLCTKEGVLLKGGKREEEKP-----FRDCADVY 290
             Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y., Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.; Sato S., Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KTAA0001-KTAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59; Mismatches 136; Indels 79; Gaps
                                                                                                                                                                                                                                                                                                PROMOTING ANGIOGENIC PROCESSES IN CERTAIN ORGANS SUCH AS AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 498;
                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 FIBRINGEN C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5D5FA63AEF6BE920 CRC64;
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COILED COIL (POTENTIAL).
FIBRINGEN C-TERMINAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROBLET, SW0146; FBC; 1.
SMART; SW0116; FBC; 1.
PROSITE; PS0514; FIBRIN_AG_C_DOMAIN; 1.
PROPPOPLED: Colled Coll; Signal; Polymorphism.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No. 1.1e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 486.5;
                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D13628; BAA02793.2; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002181; Fibrinogen_C.
MEDLINE=96051387; PubMed=7584026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      498 AA; 57513 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:484; ANGPT1.
                                                                                                                                                                                                                                                 -1- PTM: GLYCOSYLATED.
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                                                                                                                                                                                                                                                                                                                ISCHEMIC HEART
                                                                                           line KG-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 601667;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G., Koh G.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning, expression, and characterization of angiopoietin-related protein, angiopoietin-related protein induces endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JULIATION. 274:26523-26528(1999).

-!- FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN AUTOCHINE AND PARACRINE ACTION (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Secreted (By similarity).

-!- STSSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, TONGUE, LUNG AND SKELETAL MUSCLE. ALSO FOUND IN LOWER LEVELS IN KIDNEY, EPIDIDIMUS
274 GFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVG 333
                                                                                                                                                                                         347 GFGNPSGEYWLGNEFIFAITSQRQYMLRIELMDWEGNRAYSQYDRFHIGNEKQNYRLYLK 406
                                                                                                                                                                                                                                                                     334 NYNGTAGDALRFNKHYNHDLKFFTTPDDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKY 393
                                                                                                                                                                                                                                                                                                                                                407 GHTGTAGKOSSLILH-GAD---FSTKDADNDNCMC-KCALMLTGGWWFDACGPSNLNGMF 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 1 FIBRINGGEN C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                            394 YHQ-KYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    462 YTAGONHGKLNGIKWHYFKGPS-----YSLRSTTMMIRPLDF 498
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COILED COIL (POTENTIAL).
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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InterPro: IPR002181; Fibrinogen_C.
Pfam: PF00147; fibrinogen_C; 1.
SMART: SW0016; FGS; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
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164
192
493 AA;
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20.4%; Score 485.5; DB 1; Length 493;

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SEQUENCE FROM N.A. (ISOFORM GAMMA-A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
              73; Gaps
                                     66 IQLPKQFSRIEEVFKEV----QNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGA 121
                                                             170 LOLASKYKDLEHKFOHLAMLAHNOSEVIAOLEEHCORV-----PAARPMPQPPPAA 220
                                                                                      122 PGEVGD----NRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKV 177
                                                                                                                                                                262 -----TSLPSSTDKPSGP----WRDCLQALEDGHSTSSIYLVKPENTNRL 302
                                                                                                                                                                                                    221 PPRVYQPPTYNRI-----INQISTNEIQSDQNLKVLPPSLPTMPAL------ 261
                                                                                                                                       178 ANLTEVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSS 237
                                                                                                                                                                                        238 FEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKE 297
                                                                                                                                                                                                                                         298 MILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFT 357
                                                                                                                                                                                                                                                                                        358 TPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYY---HQKYRGVRNGIFWGTWPGVS 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          deoxyribonucleic acid coding for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-85252774; PubMed-2990550;
Rixon M.W., Chung D.W., Davie E.W.;
"Nucleotide sequence of the gene for the gamma chain of human
 i; Pred. No. 1.2e-25;
62; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by analysis of cDNA clones from human fetal liver.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       P02679; P04469; P04470; Q96KJ3; Q96A14; 21-JUL-1986 (Rel. 01, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Fibrinogen gamma chain precursor (PRO2061).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the gamma chain of human fibrinogen.";
Biochemistry 22:3250-3256(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chung D.W., Chan W.-Y., Davie E.W.; "Characterization of a complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-83283434; PubMed-6688357;
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                                                                                                                                                                                                                                                                                                                                           415 EAHPGGYKSSFKEAKMMIRP 434
                                                                                                                                                                                                                                                                                                                                                                  474 ----GSY--SLKKVVMMIRP 487
30.88;
              Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens (Human)
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Fetal liver;
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Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A., Cassman K.G., Goldbaum D.M., Doolittle L.R., Friezner S.J.; "The structures of fibrinogen and fibrin.";
                                                                                                                                                                                   Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.; "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Imam A.M.A., Eaton M.A.W., Williamson R., Humphries S.;
"Isolation and characterisation of cDNA clones for the A alpha- and
                                                                                                                                                                                                                                                                                                         (In) Peeters H. (eds.);
Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         splicing near the 3' end of the gene produces gamma A and gamma B forms of gamma-fibrinogen.";
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Pergamon Press, New York (1978).
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"Disulfide bridges in NH2-terminal part of human fibrinogen.";
Thromb. Res. 8:639-658(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 285-437 FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B).
MEDLINE-85030379; Pubmed-6092346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure of the human gamma-fibrinogen gene. Alternate mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wolfenstein-Todel C., Mosesson M.W.; "Carboxy-terminal amino acid sequence of a human fibrinogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marchetti L., Zanelli T., Malcovati M., Tenchini M.L.; "Polymorphism of the human gamma chain fibrinogen gene.";
                                                                         Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fornace A.J. Jr., Cummings D.E., Comeau C.M., Kant J.A.,
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Henschen A., Lottspeich F., Kehl M., Southan C.;
"Covalent structure of fibrinogen.";
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MEDLINE-83231465; PubMed~6860649;
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MEDLINE-82068993; Pubmed=7306501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma-chains of human fibrinogen.";
Nucleic Acids Res. 11:7427-7434(1983).
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                                                                                                                                                                                                                                                                                                                                                                           Pergamon Press, Oxford (1980).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 75-286 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Seq. 1:419-422(1991).
TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                     structural variants.";
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                                                                                                                                              SEQUENCE OF 27-437
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                                        Strausberg R.
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MEDLINE-84203545; PubMed-6326808; Kloczewłak M. Thimmons S., Lukas T.J., Hawiger J.; Rolezewłak M. Thimmons S., Lukas T.J., Hawiger J.; Pitatelet receptor recognition site on human fibrinogen. Synthesis and structure-function relationship of peptides corresponding to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pratt K.P., Cote H.C.F., Chung D.W., Stenkamp R.E., Davie E.W., "The primary fibrin polymerization pocket: three-dimensional structure of a 30-Kba C-terminal gamma chain fragment complexed with
Farrel D.H., Mulvihill E.R., Huang S., Chung D.W., Davie E.W.; "Recombinant human fibrinogen and sulfation of the gamma' chain."; Biochemistry 30:9414-9420(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yee V.C., Pratt K.P., Cote H.C.F., le Trong I., Chung D.W., Davie E.W., Stenkamp R.E., Teller D.C.; "Crystal structure of a 30 kba C-terminal fragment from the gamma chain of human fibrinogen.";
                                                                                                                                                                                                                       MEDLINE-85014892; PubMed-6592597;
Horwitz B.H., Varadi A., Scheraga H.A.;
"Localization of a fibrin gamma-chain polymerization site within segment Thr-374 to Glu-396 of human fibrinogen.";
Proc. Natl. Acad. Sci. U.S.A. 81:5980-5984(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human plasma fibrinogen heterogeneity: evidence for an extended
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plow E.F., Srouji A.H., Meyer D., Marguerie G., Ginsberg M.H.; "Evidence that three adhesive proteins interact with a common recognition site on activated platelets.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma-subunit positions 311 and 336 by terbium fluorescence.";
J. Biol. Chem. 260:9713-9719(1985).
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Dang C.V., Ebert R.F., Bell W.R.;
"Localization of a fibrinogen calcium binding site between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carboxyl-terminal sequence in a normal gamma chain variant
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                                                                                   EM STRUCTURE, POLYMERIZATION, AND LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
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                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-81142375; PubMed-6451630;
Olexa S.A., Budzynski A.Z.;
"Localization of a fibrin polymerization site.";
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MEDLINE=97169449; PubMed=9016719;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carboxy-terminal segment of the gamma chain.";
Biochemistry 23:1767-1774(1984).
                                                                                                                                 DOOLLULE K.F.;
"Fibrinogen and fibrin.";
Annu. Rev. Biochem. 53:195-229(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=81054908; PubMed=6933547;
Wolfenstein-Todel C., Mosesson M.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 259:5388-5391(1984).
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                                                                                                     MEDLINE=84305751; PubMed=6383194;
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                                                                                                                                                                                                        POLYMERIZATION SITE.
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                                                                                                                           Doolittle R.F.
                                                                                   REVIEW,
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MEDLINE-97134663; Pubmed-8980223;
Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
Ryan T.E., Bruno J., Radziejewski C., Maisonpierre P.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 NGMQFSTWDNDNDKF-EGNCAEQDGSGWWWNKCHAGHLNGVYYQGGTYSKASTPNGYDNG 392
                                                                                                                                                                                                                                                                                                                fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
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                                                                                                          Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F., "Crystal structure of fragment double-D from human fibrin with two
                                                                                                                                                                                                                                                                                                                                                                                                                                             8 WLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVSLPPLTIQ 67
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                  Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.; "Conformational changes in fragments D and double-D from human
                                                                                                                                                                                                                                                                                                                                                      20.4%; Score 484.5; DB 1; Length 453; 29.7%; Pred. No. 1.3e-25; tive 56; Mismatches 178; Indels 99;
                                                              X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 114-432.
MEDLINE=98292395; PubMed=9628725;
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16-OCT-2001 (Rel. 40, Last annotation update)
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  crosslinked counterpart from fibrin.";
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                                                                                                                                                                           Biochemistry 37:8637-8642(1998).
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16-OCT-2001 (Rel. 40, Last sequ
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                     Nature 389:455-462(1997).
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397 KYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437

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                                                                                                                                                                                                                            FOUND MOST PROMINENTLY IN THE HEART MYOCARDIUM SURROUNDING THE ENDOCARDIUM. LATER, IT BECOMES MORE WIDELY DISTRIBUTED, MOST OFTEN IN THE MESENCHYME SURROUNDING DEVELOPING VESSELS, IN CLOSE
                                                            TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
                                                                                                   CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRN 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 SLL------EHKILEMEGKHKEELDTLKEEKENLQGLVSRQTFIIQELEK-QLSR 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 LTDVETQVLNQTSRLEIQLLENSLSTYKLEKQLLQQTNEILKIHE-------KN 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 ATNNNSILOKQOLELMDTVHNLVSLCTKEGVLLKGGKREEEKP----FRDCADVYQAGF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 RSSETYRV----TPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGN 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62; Mismatches 141; Indels 71; Gaps
                                                                                                                                                                                      SUBCELLULAR LOCATION: Secreted.
DEVELOPMENTAL STAGE: EARLY IN DEVELOPMENT, AT E9 TO E11, IT IS
secretion-trap expression cloning.";
Cell 87:1161-1169(1996).
-!- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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COILED COIL (POTENTIAL).
FIBRINGGEN C-TERMINAL.
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                                                                                                                                                                      HEART EARLY DEVELOPMENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                      Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G.,
Koh G.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    related protein. angiopoletin-related protein induces endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 IQLPKQFSRIEEVFKEV---QNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 LOLASKYKDLEHKYQHLATLAHNQSEIIAQLEEHCORV------PSARPVPQPPPAA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 PGEVGD----NRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning, expression, and characterization of angiopoietin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, SMALL INTESTINE, SPLEEN AND STOWAGH. ALGO FOUND IN LOWER LEYELS IN COLON, OVARY,
                                                                                                                                                                                                                                                     Mammalia, Butheria, Primates, Catarhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7. Biol. Chem. 274:26523-26528(1999).
--- FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN
AUTOCRINE AND PARACRINE ACTION.
                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
15-UNV-XOOZ (Rel. 41, Last annotation update)
Angiopoietin-related protein 2 precursor (Angiopoietin-like 2):
ANGPPL2 OR ARP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.2%; Score 480.5; DB 1; Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANGIOPOIETIN-RELATED PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: CONTAINS 1 FIBRINGEN C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADRENAL GLAND, SKELETAL MUSCLE AND IN PROSTATE.
466 ONHCKENGIKWHYFKGPS-----YSLRSTTMMIRPLDF 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .7e-25
                                                                                                 493 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1. Signal; Coiled coil; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99403103; PubMed=10473614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002181; Fibrinogen_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00147; fibrinogen_C; 1. SMART; SM0186; FBG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF125175; AAD55357.1; -.
                                                                                                                                       .6-OCT-2001 (Rel. 40, Created)
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                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: N-GLYCOSYLATED.
                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                 ANL2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sprouting.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETTA AND GAMAA), LINKED TO EACH OTHER BY DISULETURE BONDS.
-1- MISCELLANBOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES, FIBRINOPEFTIDES A AND B FROM ALPHA & BETA
                                                                                        178 ANLTFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSS 237
                                                                                                                                                262 ------TSLPSSTDKPSGP-----WRDCLQALEDGHDTSSIYLVKPENTNRL 302
                                                                                                                                                                                                                                                                                                                                                    303 MQVWCDQRHDPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNOGN 362
                                                                                                                                                                                                                                                                                                                                                                                                                                        298 MILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : :||::| :::| | | : | |:| |:| ||: | |:| |:| ||:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 TPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYY---HQKYRGVRNGIFWGTWPGVS 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 FEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKE 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Amino acid sequences of lamprey fibrinopeptides A and B and characterizations of the junctions split by lamprey and mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragments).
Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bohonus V.L., Doolittle R.F., Pontes M., Strong D.D.;
"Complementary DNA sequence of lamprey fibrinogen beta chain.";
Biochemistry 25:6512-6516(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 1 FIBRINGEN C-TERMINAL DOMAIN.
221 PPRVYQPPTYNRI-----INQISTNEIQSDQNLKVLPPPLPTMPTL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               477 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochim. Biophys. Acta 453:426-438(1976).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415 EAHPGGYKSSFKEAKMMIRP 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 474 ----GSY ---SLKKVVMMIRP 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-36.
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66; Mismatches 138; Indels 113; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 ELREELLKQRDPVR------YKISMLK-------QNLTYF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 VNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVRELESEVNKLSSELKNAK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 -----VQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 CTVNCRVPVVSGMHCEDIYRNGGRISEAYYIQPDLFSEPYKVFCDMESHGGGWTVVQNRV 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 NGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDAL-----RFNKHYN-HDLKFFTT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 EGSSVYAQYASFRPENEAQGYRLWVEDYSGNAGNALLEGATQLMGDNRTMTIHNGMQFST 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 INSFDR------MASDSNTLKQN------VQTLRRRLNSRSSTHVNAQ 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 EEINVLHGRLEKLNLVNMNNIENYVDSKVANLTFVVNSLDGKCSK----CPSQEQIQSRP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 DGSTNFTRTWQDYKAGFGNLR------REFWLGNDKIHLLTKSKEMILRIDLEDF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 PDKDNDRY----PSGNCGLYYSSGWWFDACLSANLNGKYY-----HOKYRGVRNGIFW 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 EIKDERAKDVCPVRLESRGKCEEAGECPYQVSLPPLTIQLPKQFSRIEEVFKEVQNLKEI 88
                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. ..).
INTERCHAIN (WITH THE ALPHA CHAIN)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERCHAIN (WITH THE GAMMA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN (WITH THE ALPHA CHAIN) (BY SIMILARITY).
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.2%; Score 479.5; DB 1; Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B8A95E7E32D09D18 CRC64;
                                                                                                                                         PROSITE; PS00514; FIBRIN AG_C_DOMAIN; 1.
Blood coagulation; Plasma; Sulfation; Glycoprotein.
                                                                                                                                                                                                                                                                        FIBRINOGEN BETA CHAIN.
                                                                                                                                                                                                          FIBRINOPEPTIDE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY)
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BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                    IPR002181; Fibrinogen_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412 425 b
477 AA; 54270 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131; Conservative
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84
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                                                                                                               SMART; SM00186; FBG;
PIR; A03124; A03124
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                                                       HSSP; P02675; 1FZF
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                                                                                    InterPro;
                                                                                                                                                                                                                                        NON_CONS
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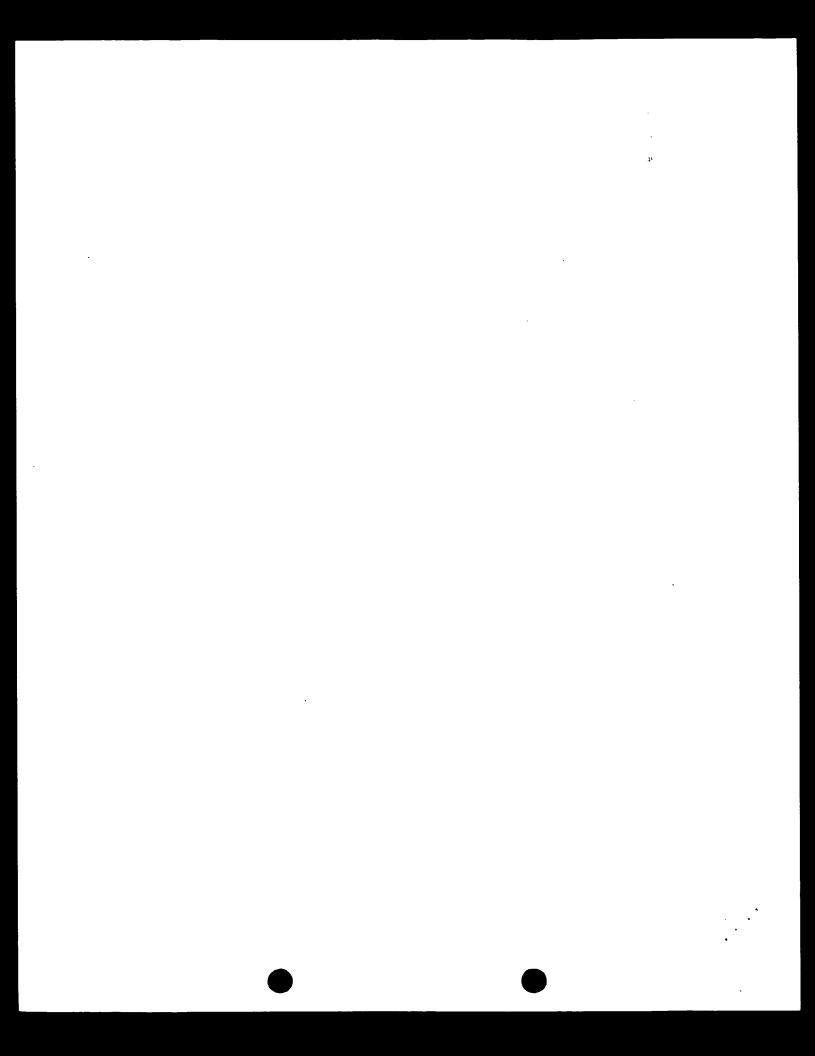
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :. Natl. Acad. Sci. U.S.A. 78:1466-1470(1981).
FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETTA AND GAMMA), LINKED TO EACH OTHER BY DISULEIDE BONDS.
-1- MISCELLANBOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XIIIA WHICH CATALYZES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-81199473; PubMed-6262803; Chung D.W., Rixon M.W., McGillivray R.T.A., Davie E.W.; "Characterization of a cDNA clone coding for the beta chain of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BETWEEN GAMMA CHAINS
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                 MEDLINE-79164394; PubMed=434821; Marthelli R.A., Inglis A.S., Rubira M.R., Hageman T.C., Marthell J.G.R., Leach S.J., Scheraga H.A.; "Amino acid sequences of portions of the alpha and beta chains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMM (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfation.
                                                                                                                                             "The sequence of amino acids at the N-terminal end of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLEAVAGE (BY THROMBIN; RELEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIBRINGEN BETA CHAIN.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 FIBRINGEN C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN (WITH ALPHA). INTERCHAIN (WITH ALPHA).
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INTERCHAIN (WITH ALPHA).
INTERCHAIN (WITH GAMMA).
                                                                                                                                                                                                                          Sjoguist J., Blomback B., Wallen P.;
"Amino acid sequence of bovine fibrinopeptides.";
Ark. Kemi 16:425-436(1960).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIBRINOPEPTIDE B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIBRINOPEPTIDE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                     Arch. Biochem. Biophys. 192:27-32(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00514; FIBRIN_AG_C_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SULFATION.
                                                                                                                                                                             Acta Chem. Scand. 17:1816-1819(1963).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002181; Fibrinogen_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00147; fibrinogen_C; 1.
                                                                                                                           Blomback B., Doolittle R.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; V00110; CAA23444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 44-468 FROM N.A.
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83
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Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                  fibrinogen.
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                                                                                                                                                                                                                                                                                                  SEQUENCE OF 22-53.
                                                                                                                                                            fibrinopeptide B.
                                                                                                                                                                                                                SEQUENCE OF 5-21
                                                                        NCBI_TaxID=9913;
                                                                                                          SEQUENCE OF 1-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGREGATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fibrinogen.";
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57; Mismatches 149; Indels 86; Gaps
                                                                                                                                                                                         61 LPPLTIQLPKQFSRIEE-VFKEVQNLKEIVNSLKKSCQDC--KLQADDNGDPGRNGLLLP 117
                                                                                                                                                                                                               118 STGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKV 177
                                                                                                                                                                                                                                                                                                     136 -----QNQVQDNENVVNEYSS------HLEKHQLYIDETVKNNIPTKL 172
                                                                                                                                                                                                                                                                                                                                         178 ANLTEVVNSLDGKCSKCPSQEQIQSR------PVQHLIYKDCSDYYAIGKRSSE 225
                                                                                                                                                                                                                                                                                                                                                                            173 RVLRSILENLRSKIOKLESDVSTOMEYCRTPCTVTCNIPV--VSGKECEKIIRNEGETSE 230
                                                                                                                                                                                                                                                                                                                                                                                                                  226 TYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRR---- 280
                                                                                                                                                                                                                                                                                                                                                                                                                                        281 -----EFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 KYCGVPGEYWLGNDRISQLTNMGPTKLLIEMEDWKGDKVTALYEGFTVQNEANKYQLSVS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 NYNGTAGDAL-----RFNKHYN-HDLKFFTTPDKDNDRY----PSGNCGLYYSSGWW 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 KYKGTAGNALIEGASQLVGENRTMTIHNSMFFSTYDRDNDGWKTTDPRKQCSKEDGGGWW 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 FDACLSANLNGKYY-----HQKYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIR 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 96:1904-1909(1999).
-!- FUNCTION: BINDS TO TYROSINE-PROTEIN KINASE RECEPTOR TIE2 AND MAY ACT AS AN ANTAGONIST.
-!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
-!- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
-!- CAUTION: WAS ORIGINALLY (REF.1) CALLED ANGIOPOLETIN-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Valenzuela D.M., Griffiths J.A., Rojas J., Aldrich T.H., Jones P.F., Zhou H., McClain J., Copeland N.G., Gilbert D.J., Jenkins N.A., Huang T., Papadopoulos N., Maisonpierre P.C., Davis S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Angiopoietins 3 and 4: diverging gene counterparts in mice and
                                                            .) (PROBABLE).
                                                                                                                  DB 1; Length 468;
                                      BY SIMILARITY.
N-LINKED (GLCNAC. . .) (Pl
                                                                                                                                    Pred. No. 1.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
    BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiopoietin-4 precursor (ANG-4) (ANG-3).
ANGPT4 OR AGPT4 OR ANG3.
                                                                                                                19.8%; Score 471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Myoblasts, and Uterus;
MEDLINE=99162530; Pubmed=10051567;
208 293 BY
218 247 BY
401 414 BY
371 N-L
468 AA; 53340 MW; 2
                                                                                                                                  30.6%;
                                                                                                                                                    129; Conservative
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                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yancopoulos G.D.;
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                                                        CARBOHYD
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78; Gaps 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 RLQALEAQHQAQLNSLQEKREQLHSLLGHQTGTLANLKHNLHALSSNSSSLQQQQQLTE 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 QLPKQFSRIEEVFK-EVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGA---- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 PGEVGDNRVRELESEV----- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 QTKAQTHKLTAVEAQVLNQTLHMKTQMLENSLSTNKLERQMLMQSRELQRLQGRNRALET 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 ----LEKLNLVNMNNIE------NYDSKVANLTFVVNSLDGKCSKCPSQEQIQSR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 PVQHL------IYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDME 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 FVQRLVRIVAQDQHPVSLKTPKPVFQDCAEIKRSGVNTSGVYTIYETNMTKPLKVFCDME 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 IMGGGWIVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 DFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDNDR 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 YPSGNCGLYYSSGWWFDACLSANLNGKYY--HQKYRGVRNGIFWGTWPGVSEAHPGGYKS 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.8%; Score 470.5; DB 1; Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 29.0%; Pred. No. 1.3e-24;
Matches 125; Conservative 74; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      9B5A74A20A6664F6 CRC64;
                                                                                                                                                                                                                                                                                                                                        ANGIOPOIETIN-4.
COILED COIL (POTENTIAL).
FIBRINGEN-LIKE.
                                                                                                                                                                                                                                                                              PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
                                                                                                                                                                                                  MGD; MGI:1336887; Agpt4.
InterPro; PRR003181; Fibrinogen_C.
Pfam: PF00147; fibrinogen_C; 1.
SMART; SM00186; FBG; 1.
                                                                                                                                                             EMBL; AF113707; AAD21586.1; -.
                                                                                                                                                                                                                                                                                                                                                         181 269 C
294 480 F
509 AA; 57805 MW;
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509
269
480
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Search completed: December 2, 2002, 06:51:11 Job time: 38.7445 secs

500 ----TRMMLRP 506



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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

December 2, 2002, 06:48:20 ; Search time 119.903 Seconds (without alignments) 754.398 Million cell updates/sec Run on:

US-09-902-563-2 2378

1 MKLANWYWLSSAVLATYGFL.....GYKSSFKEAKMMIRPKHFKP 439 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapext 0.5

671580 seqs, 206047115 residues Searched:

671580 tal number of hits satisfying chosen parameters:

Annimum DB seq length: 0
Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database :

SPTREMBL_21:* l: sp_archea:* 2: sp_bacteria:* sb_fundi:*

sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:* sp_rodent:*
sp_virus:*
sp_vertebrate:* sp_organelle:*
sp_phage:*
sp_plant:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	09ept7 rattus norv	O8wwe4 homo sapien	Ognđal ciona intes	O8t8a2 ciona savid	09d2d2 mus musculu	Ogderl dallus dall	Ogder0 gallus gall	Ogder2 gallus gall	Ogo2v7 homes anien	090u54 dallus dall	O9bdv7 sus scrofa	OBVC25 mis miscuili	095841 homo sapien	Oghba homo sanien	090z19 hrachydanio	Q8r1q3 mus musculu
ID	Q9EPT7	Q8WWE4	Q9NDQ1	Q8T8A2	Q9D2D2	Q9DER1	Q9DERO	Q9DER2	09P2Y7	Q9PU54	Q9BDY7	Q8VC25	095841	09HBP3	090219	Q8R1Q3
DB	Ξ	4	'n	'n	11	13	13	13	4	13	9	11	4	4	13	11
Query Match Length DB	357	148	652	220	496	407	441	493	495	407	496	314	491	244	513	337
Query Match	69.3	31.5	26.0	25.0	22.1	22.0	22.0	22.0	22.0	22.0	22.0	21.8	21.2	20.9	20.7	20.6
Score	1647	750	618.5	593.5	526	524	524	524	523.5	523	523	518.5	505	496	491.5	491
Result No.	-	2	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16

043827 homo sapien Q948w8 tachypleus Q91589 xenopus lae Q91j03 rattus norv Q998w6 tachypleus	Q9bdy8 sus scrofa Q9bdy8 sus scrofa Q90z18 brachydanio Q9u8w7 tachypleus Q95p99 halocynthia		Q9bz20 homo sapien Q9bz20 homo sapien Q9be00 macaca fasc Q28763 papio cynoc Q28763 papio cynoc Q29042 sus scrofa Q95pa0 halocynthia	Q29041 sus scrofa Q28529 mustela put Q00546 gallus gall Q00531 homo sapien Q27752 homo sapien Q15568 homo sapien Q28703 oryctolagus
043827 Q9U8W8 Q91589 Q9JJ03 Q9U8W6	Q9BDY8 Q90Z18 Q9U8W7 Q95P99	Q95LU3 Q95P98 Q8WUR3 Q8VCM7	Q9EZZQ Q9EZZQ Q28763 Q29042 Q9CU50	Q29041 Q28529 Q00546 000531 Q92752 Q15568
4 13 11 5	2022	924	111	m
346 292 488 493 308	4489 316 324 341	4331 436 436 436	337 337 326 326 279	323 316 1353 712 1358 1358
200.0 200.3 200.0 200.0	199.00	19.1 18.8 18.8	18.3 18.3 18.3 18.3	18.0 18.0 17.8 17.7 17.7 17.7
489 485.5 482.5 481.5 476	474.5 473 471 456.5 456	454.5 454. 448 448	439.5 437.5 434.5 433.5	428.5 427 423 421 421 421 420.5
17 18 19 20 21	23 25 26 27	28 30 32 32	33 34 35 37 38	44 44 45 45

ALIGNMENTS

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			tomi; ;; Rattus.										8; Gaps	VRELE 134	VQELE 52	KCSKC 194	KCFKC 112	GWTVL 254
	-		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus NCBI TaxiD-10116;				databases.				C64;	Length 357;	Indels	IEBVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVRELE	HILLIH HILL HILLIH HILI	SEVINELSSELKNAKEEINVEHGREEKINIVINININIENYVDSKVANLTFVVNSLDCKCSKC	SQVNKLSSELKNAKEEIQGLQGRLESLQLVNMNNIENYVDNKVANLTSVVNSLDSKCFKC	PSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVL 254
357 AA.	Created) Last sequence update) Last annotation undate)		Vertebrata hi; Murida			at.";					:00514; FIBRIN_AG_C_DOMAIN; 1. 357 AA; 40966 MW; 31183DD9A02EBBA9 CRC64;	DB 11;	.9e-100; es 31;	GRNGLLLPST	GGNG	ENYVDSKVAN	ENYVDNKVAN	TPDPKNSSFE
PRT; 357	Created) Last sequence update) Last annotation updat		Sraniata; Sciurognat			KYCHIIK D.F., Chien E., Phillippe M.; "FGL2 Expression in the Spraque-Dawlev Rat.";	Submitted (AUG-2001) to the EMBL/GenBank/DDBJ FMBL: AF323608. AAG42269 1.		٦ <u>-</u> c.	SMART; SM00186; FBG; 1.	OOMAIN; 1. 31183DD9A	Score 1647; DB 11;	best botal similarity 62.7%; Fred. No. 3.98-100; Matches 302; Conservative 24; Mismatches 31;	KLQADDNGDF	(LQADEHPDF	CLNEVNMNNI	SLOLVIMNI	KRSSETYRV
	16, 16, 19,	E).	Chordata; C Rodentia;		1	., Phillig he Spraque	to the EMI		Fibrinoger	1.	RIN_AG_C_I 1966 MW;		oz./*; F1 :ive 24;	SLKKSCQDCF	SLKKSCQDCF	INVLHGRLER	TOGLOGRLES	KDCSDYYAIG
PRELIMINARY;	(TrEMBLrel. (TrEMBLrel.	Prothrombinase FGL2. Rattus norvegicus (Rat).	etazoa; Cl theria; Rc 0116;	N.A.	STRAIN-SPRAGUE-DAWLEY;	RYCLLIK D.F., Chien E., "FGL2 Expression in the	Submitted (AUG-2001) to the EME FMRT. AF323608: AAG42269 1: -	; 1FZD.	InterPro; IPR002181; Fibrinogen_C. Pfam: PF00147. fibrinogen_C. 1	36; FBG;]	0514; FIBE 57 AA; 4(Conservati	VONLKEIVNS	VRTLQEAVDS	SELKNAKEET	SELKNAKEEJ	SRPVQHLIYE
	2001 2001 2001	Prothrombinase FGL2 Rattus norvegicus (Eukaryota; Metazoa; Mammalia; Eutheria; NCBI TaxID=10116;	[1] SEOUENCE FROM N.A.	AIN-SPRAGE	niik D.F. L2 Expres:	mitted (A	HSSP; P02671; 1FZD.	erPro; IP	RT; SM0018	PROSITE; PSO(SEQUENCE 35	Query Match	s 302; (75 IEEVFKEN	1 MEEVLKEN			
RESULT 1 Q9EPT7 ID Q9EPT7			OC Mamy				RL Subr		DR Inte		DR PROS	Query Match	Matche	Qy 75	Db 1	Qy 135	Db 53	Qy 195

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Satoh N.;
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33 VYDQFYVANEFLKYRLHLGNYNGTAGDALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLY 292
                                                                                                                                                                                                   293 YSSGWWFDACLSANLNGKYNQRYKGVRNGIFWGTWPGVSQAHPGGYKFSFKKAKMMIRP 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG 120
                                                  255 QARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYA 314
                                                                                                                     315 LYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLY 374
                                                                                                                                                                                      375 YSSGWWFDACLSANLNGKYYHQKYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRP 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLANWYWLSSAVLAAYGFLVVANNETEEIKDERAKDVCPVRLESRCKCEEAGECPYQVS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ciona intestinalis.
Bukhryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
NCBI_TaxID=7719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.5%; Score 750; DB 4; Length 148
99.3%; Pred. No. 6.4e-42;
v'·mmatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; BC017813. AAH17813.1; -.
InterPro: JFR001899; Gram_pos_anchor.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 148 AA; 16561 MW; 456B7DBA37C07F21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEWBLrel. 20, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Similar to fibrinogen-like 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                      435 KHFKP 439
                                                                                                                                                                                                                                                                                      353 KSFKP 357
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'Characterization of Brachyury downstream notochord genes in the Ciona
                  Hotta K., Takahashi H., Asakura T., Saitoh B., Takatori N., Satou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 NYVDSKVANLT----FVVNSLDG-----KCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 NYIYSEGSGVNIRDGYATNETEGIEFTSRILRATNPTPVQDGQTESLPY-DCAELYARGV 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 RSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRRE 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 FWLGNDKIHLLT---KSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGT 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              489 HWIGLEKMHHISTSNKSRRMELRINLTDWDDVSHYANYGVFRIRSEGKNYQLIAKRYTGT 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 AGDALRENKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKY 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     549 AGDALNYGENYNHHLQPFTTFDRDNDGYALGNCGRYYRSGWWFNACFAANLNGNYYTGPY 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 YRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGN 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 DKIHLLT----KSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDAL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 YEIKPN-TDETWMYYCDMETAGGGWTVIQKRVDGEENFSRNWKAYKNGFGDKNKDHWIGL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Early embryonic expression of FGF4/6/9 gene and its role in the induction of mesenchyme and notochord in Ciona savignyi embryos."; Development 129:1729-1738(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.0%; Score 618.5; DB 5; Length 652; 43.0%; Pred. No. 1.8e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.0%; Score 593.5; DB 5; Length 220;
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                                                                                                                                   intestinalis embryo.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, ABG036849; BAB006546.1; -
                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SEQUENCE 652 AA; 73252 MW; A492BA325162F0E0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Fibrinogen-like protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399 RGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 43.08; Pred. No. 1.8e
Matches 120; Conservative 53; Mismatches
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Imai K.S., Satoh N., Satou Y.;
                                                                                                                                                                                                                                                                           InterPro; IPR002181; Fibrinogen_C.
Pfam; PF00147; fibrinogen_C; 1.
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                                                                                                                                                                                                                                                                                                                                                   SM00186; FBG; ]
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                                                                                                                                                                                                                                             HSSP; P02671; 1FZD.
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SEQUENCE FROM N.A
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MEDLINE=20422311; PubMed=10964717;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ289778; CAC08175.1; -. HSSP; P02671; 1FZD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
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RA ATAKWA T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA ATAKWA T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA ATAKWA T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
ATAKWA T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A ATAKWA T., Hara A., Shibata K., Yoshino M., Radchi J., Fekuda S.,
RA Aizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa M., Jawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito T., Okazaki Y., Globori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda T., Gissi C., King B., Rochiwa H.,
Rubil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bassh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.,
Blake J., Boffelli D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
Lyons P., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Wynshaw-Boris A., Yoshida K., Wasegawa Y., Kawaji H., Kohtsuki S.,
Anashisaki V.
                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, clone:5031400E18, full insert sequence (Angiopoietin
                                                     344 RFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVRN 403
 63. ERMHHLTTSNKSRRLKLRIDLIDWDDVNHYAEYETFRVRGEGKNYQLIAKKFSGTAGDAL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 APGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRL-----EKLNLVNMNNIENY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40; Gaps
                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK019860; BAB31887.1; -.
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496 AA; 56575 WW; E7563B498A0EF331 CRC64;
                                                                                                                          183 GIYWGTWYKLSDSRSNA-RYSFKYVDMKVRPLNFE 216
                                                                                                    404 GIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHFK 438
                                                                                                                                                                                                                          496 AA.
                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                            PRT;
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InterPro; IPR002181; Fibrinogen_C.
Pfam; PF00147; fibrinogen_C; 1.
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                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                  173 VDSKVANLTFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPD 232
                                                                                                                                                                           244 LOKQOHDLMETVNSLLTMMSSPNSKSSVAIRKEEQTTFRDCAEIFKSGLTTSGIYTLTFP 303
                                                                                                                                                                                                                                        233 PKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLL 292
                                                                                                                                                                                                                                                                                                                                                                                    293 TKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHD 352
                                                                                                                                                                                                                                                                                                                                                                                                                                  ANĞIOPOIETIN-2B.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353 LKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWP 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423 ---FSTKDSDNDKCIC-KCSQMLSGGWWFDACGPSNLNGQYYPQKQNTNKFNGIKWYYWK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 EKRVLEMEDKHTLOLKSIKDEKDQLQVLVARQNSIIEELEKQLVTATVNNSVLQKQQHDL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 DSKVAN-LIFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPD 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 METVHNLLTMISTPNSAKKNFIAKEEQIS-----FKDCAEAFKSGLTTSGIYTLIFP 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 PKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 NSAQEKKAYCDMESNGGGWTVLQRREDGSVDFHRTWKEYKIGFGDPAGEYWLGNEFVSQL 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mezquita J., Mezquita P., Montserrat P., Mezquita B., Francone V., Vilagrasa X., Mezquita C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam: PF00147; fibrinogen_C; 1...
MARRY: SM00186; FBG; 1...
PROSITE; PS00514; FTBR1...
SEQUENCE 407 AA; 46687 WW; 8863BAQABBC7A41C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 275:643-651(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       479 G-----SGY--SLKATTMMIRPADF 496
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"Biologic significance of angiopoietin-2 expression in human
01-WAR-2001 (TrEWBLrel. 16, Created)
01-WAR-2001 (TrEWBLrel. 16, Last sequence update)
01-DEC-2001 (TrEWBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412 GVSEAHPGGYKSSFKEAKMMIRPKHF 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476 G----SGY--SLKATTMMIRPADF 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                    IPR002181; Fibrinogen_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99126459; PubMed=9927494;
                                                                                                                                                                                                                                                                                                                  PF00147; fibrinogen_C; 1
                                                                                                                                                                                                                                                                     EMBL; AJ289777; CAC08174.1;
HSSP; P02671; 1FZD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                 SMART; SM00186; FBG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                               Angiopoletin-2A.
                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606
                                                             ANGIOPOIETIN-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angiopoietin-2
                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9P2Y7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
    δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 ---FSTKDADNDKCIC-KCSQMLTGGWWFDACGPSNLNGMYYPLRQNNNKFNGIKWYYWK 423
                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 DNRVRELESEVNKLSSELKNAKEEINVLHGR------LEK-LNLVNMNNI-----ENYV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 PKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 NSAQEKKAYCDMESNGGGWTVLQRREDGSVDFHRTWKEYKIGFGDPAGEYWLGNEFVSQL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 TKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHD 352
                   353 LKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWP 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 EKRVLEMEDKHTLQLKSIKDEKDQLQVLVARQNSIIEELEKQLVTATVNNSVLQKQQHDL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 DSKVAN-LTFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPD 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 TNOKRYVLKIILKDWEGNEAYTLYDQFYLANEEOKYRIHLKGLTGTAGKISSISQPGND- 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 LKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWP 411
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                                                                                                                                                                                                                                                                                                                                                                                                            Mezquita J., Mezquita P., Montserrat P., Mezquita B., Francone V., Vilagrasa X., Mezquita C.;
"Genomic structure and alternative splicing of chicken angiopoietin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.0%; Score 524; DB 13; Length 441; 38.3%; Pred. No. 1.6e-26; tive 45; Mismatches 120; Indels 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DC98127FE0CE34E2 CRC64;
                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Commun. 275:643-651(2000).
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                                                                                                                                                                                    PRT; 441 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00186; FBG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                            412 GVSEAHPGGYKSSFKEAKMMIRPKHF 437
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                                                                                                         390 G----SGY--SLKATTMMIRPADF 407
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20422311; PubMed=10964717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR002181; Fibrinogen_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441 AA; 50472 MW;
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EMBL; AJ289779; CAC08176.1; --
HSSP; P02671; 1FZD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00147; fibrinogen_C; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                           Anglopoletin-2C
                                                                                                                                                                                                                                                                        ANGIOPOIETIN-2C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125;
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Q9DER2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                    Q9DER0
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36; Gaps 10;
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 DNRVRELESEVNKLSSELKNAKEEINVLHGR-----LEK-LNLVNMNNI-----ENYV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 EKRVLEMEDKHTLQLKSIKDEKDQLQVLVARQNSIIEELEKQLVTATVNNSVLQKQQHDL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 METVHNLLTMISTPNSAKKNFIAKEEQIS-----FKDCAEAFKSGLTTSGIYTLTFP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 PKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLL 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 DSKVAN-LTFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPD 232
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-20422311: Pubmed-10964717;
MEZGUIGA J., Mezquita P., Montserrat P., Mezquita B., Francone V.,
Vilagrasa X., Mezquita C.;
"Genomic Structure and alternative splicing of chicken angiopoietin-
"Genomic structure and alternative splicing of chicken angiopoietin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 22.0%; Score 524; DB 13; Length 493; Best Local Similarity 38.3%; Pred. No. 1.9e-26; Matches 125; Conservative 45; Mismatches 120; Indels 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanaka S., Mori M., Sakamoto Y., Makuuchi M., Sugimachi K.,
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SEQUENCE 493 AA; 56393 MW; BD1A21F90172F6DA CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 275:643-651(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 VNNLLTMMSTSNSKDPTVAKEEQ-ISFRDCAEVFKSGHTTNGIYTLTFPNSTEEIKAYCD 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 METMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRID 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374 LKDWEGNEAYSLYEHFYLSSEELNYRIHLKGLTGTAGKISSISQPGND----FSTKDGDN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364 DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 DKCIC-KCSQMLTGGWWFDACGPSNLNGMYYPQRQNTNKFNGIKWYYWKG-----SGY- 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----NMNNIENYVDSKVANLTF-----V 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 VLAMEDKHIIQLQSIKEEKDQLQVLVSKQNSIIEELEKKIVTATVNNSVLQKQQHDLMET 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                               Match 22.0%; Score 523.5; DB 4; Length 495; Local Similarity 28.1%; Pred. No. 2e-26; Less 139; Conservative 76; Mismatches 155; Indels 125; Gaps
                                                                                                                                                                                                                                                                                                                                                                                             85 LKE-----IVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN---- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                      86 IMENNTOWLMKLENYIQDNMKKEMVEIQQNAVQN-------OTAVMIEIGTNLLNQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 -----RVRELESEV----LEKL 161
                                                                                                                                                                                                                                                                                                          43 LESRGKCE---EAGECPYQVSLPPL------TIQ--LPKQFSRIEEVFKEVQN 84
                                                                                                                                                                                                                                                                                                                                                26 MDSIGKKQYQVQHGSCSYTFLLPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLEN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99333704; PubMed=10403795; Mezquita J., Mezquita J., Mezquita B., Pau M., Mezquita C.; Mezquita J., mezquita B., Pau M., Mezquita C.; Mezquita Inovel form of angiopoietin-2 (Ang-2B) and expression of VEGF and angiopoietin-2 during chicken testicular development and regression.";
                                                                                                                                                                       495 AA; 56848 MW; EBFAC35ABF1F08F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                 PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1
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                J. Clin. Invest. 103:341-345(1999).
EMBL; AB009865; BAA95590.1;
                                                                              InterPro; IPRO02181; Fibrinogen_C. Pfam; PF00147; fibrinogen_C; 1. SMART; SM00186; FBG; 1.
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hepatocellular carcinoma.";
                                                                                                                                                                                                                                                            Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Angiopoietin-2B (Ang-2B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            482 -SLKATTMMIRPADF 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                              P02671; 1FZD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 NLV----
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                    Query Match
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36; Gaps 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 DNRVRELESSEVNKLSSELKNAKEEINVLHGR-----LEK-LNLVNMNNI-----ENYV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 METVHNILTMISTPNSAKKNFIAKEEQIS-----FKDCAEAFKSGLTTSGTYTLTFP 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 PKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 TKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHD 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 TNOKRYVLKIILKDWEGNEAYTLYDQFYLANEEQKYRIHLKGLTGTAGKISSISQPGND- 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 LKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWP 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |---FSTKDTDNDKCIC-KCSQMLTGGWWFDACGPSNLNGMYYPLRQNNNKFNGIKWYYWK 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim I., Moon S.O., Han C.Y., Pak Y.K., Moon S.K., Kim J.J., Koh G.Y., "The angiopoietin-tie2 system in coronary artery endothelium prevents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 DNRVRELESEVNKLSS------ELKNAKEEINVLHGRLEKLNLVNMNN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 EKRVLEMEDKHTLQLKSIKDEKDQLQVLVARQNSIIEELEKQLVTATVNNSVLQKQQHDL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 DSKVAN-LTFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPD 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                        22.0%; Score 523; DB 13; Length 407; 38.3%; Pred. No. 1:7e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                      45; Mismatches 120; Indels
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PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SEQUENCE 496 AA; 56911 MW; 33B02BE224FE6B9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oxidized low-density lipoprotein-induced apoptosis.";
Cardiovasc. Res. 49:872-881(2001).
EMBL; AF233228; AAK14993.1; -.
                                                                                                                                                                                                                                                                   407 AA; 46647 MW; E10C03D07E410013 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Biochem. Biophys. Res. Commun. 260:492-498(1999).
EMBL; AJ131923; CAB59200.1; -.
HSSP; P02671; 1FZD.
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                                                                                                                                                                                                                   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1 SEQUENCE 407 AA; 46647 MW; E10C03DO
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Pfam; PF00147; fibrinogen_C; 1.
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                                                                                                                 InterPro; IPR002181; Fibrinogen_C. Pfam; PF00147; fibrinogen_C; 1.
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                                                                                                                                                                                                  SMART; SM00186; FBG; 1
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Best Local Similarity.
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231 EKQLVTATVNNSVLQKQQHDLMETVHNLLTMISTSNSAKHSLVAKEEQI-----IFR 282
  ------LIFVVNSLDGKCSKCPSQEQIQSRPVQHLIYK 211
                                                                                                  403 LKGLTGTAGKISSISQPGND---FSTKDADNDKCIC-KCSQMLTGGWWFDACGPSNLNG 457
                                                                         212 DCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDY 271
                                                                                                                                                       272 KAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLH 331
                                                                                                                                                                                                                                 332 VGNYNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNG 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 VIPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNL---RREFWLG 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.8%; Score 518.5; DB 11; Length 314; 37.0%; Pred. No. 2.4e-26; tive 42; Mismatches 116; Indels 57;
                                                                                                                                                                                                                                                                                                           392 KYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437
                                                                                                                                                                                                                                                                                                                                                458 MYYPQRQNTNKFNGIKWYYWKG-----SGY--SLKATTMMIRPADF 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021946; AAH21946.1; -
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Pfam; PF00147; fibrinogen_C; 1.
SMART; SM00186; FG1.
PROSTIE: PS00514; FIBRIN AG_DONAIN; UNKNOWN 1.
SEQUENCE 314 AA; 36439 MW; 52C16CA9C2D0386A CRC64;
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(TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
169 IENYVDSKVAN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
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Kim I., Kwak H.J., Ahn J.E., So J.N., Liu M., Koh K.N., Koh G.Y.; "Molecular cloning and characterization of a novel angiopoietin family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 21.2%; Score 505; DB 4; Length 491;
Best Local Similarity 26.9%; Pred. No. 3.3e-25;
Matches 131; Conservative 81; Mismatches 137; Indels 138; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 GK-EEAKKCAYTFLVPEQRITGPICVNTKGQDASTIKDMITRMDLENLKDVLSRQKREID 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 DCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 VLQLVVDVDGN-------IVAEVKLIRKESRNMNSRVTOLYMO 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 L-----EKLNLVNMNNIENYV--------L 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 LLHEIIRKRDNSLELSQLENKILNVTTEMLKMATRYRELEVKYASLTDLVNNQSVMITLL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 GKCEEAGECPYQVSLPPLTIQLP-----KQFSRIEEVF--KEVQNLKEIVNSLKKSCQ 97
                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ito Y., Oike Y., Yasunaga K., Matsumoto S., Ota T., Nishikawa T.,
Kawai Y., Isogai T., Hamada K., Saito Y., Miyata K., Masuho Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ota T., Nishikawa T., Kawai Y., Suzuki Y., Ishii S., Saito K., Yamanoto J., Sugano S., Isogal T.; "HRI human cDNA sequencing project."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                               01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Angiopoletin (TrEMBLrel. 17) Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB 2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF107253; AAD19608.1; -.
EMBL; AL355520; CAC13169.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3C4DB8DEF6CF7E99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 DGKCSKCPSQEQIQSRP-----VQHL-------
                                      491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
                                      PRT;
                                                                                                                                                                                                                                                                                                                      MEDLINE=99148829; PubMed=10025962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro, IPR002181; Fibrinogen_C. Pfam; PF00147; fibrinogen_C; 1. SMART; SM00186; FBG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB056476; BAB40691.1; -. HSSP; P02671; 1FZD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN 24 491 PH SEQUENCE 491 AA; 56719 MW;
                                                                                                                                                                                                                                                                                                                                                                             protein, angiopoletin-3.";
FEBS Lett. 443:353-356(1999).
                                                                                           (TrEMBLrel. 10,
                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                    DJ595C2.2 OR ARP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=PLACENTA;
                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein (ARP4).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                      TISSUE=HEART
                                                                                           01-MAY-1999
                                                                                                                                                    precursor).
                                                        095841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
RESULT 13
                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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                                                                                                                                                                                                                                                             177 VANLTFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 SFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 EIKAYCDMEAGGGGWTIIQRREDGSVDFQRTWKEYKVGFGNPSGEYWLGNEFVSQLTNQQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 EMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFF 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : |||::|| : || | : || | 431 NCAHFHKGGWWYNACAHSNLNGVWYRGGHYRSKHQDGIFWAEYRG-----GSY--SLRA 482
250 GWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNG 309
                                                                                                                                                                                                                                310 VELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYPSG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.9%; Score 496; DB 4; Length 244;
38.9%; Pred. No. 5.1e-25;
Live 43; Mismatches 95; Indels 22; Gaps
                                                               ----IYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGG 249
                                                                                                    257 TSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIYMIKPENSNGPMQLWCENSLDPG 316
                                                                                                                                                                                                                                                                                                                     370 NCGLYYSSGWWFDACLSANLNGKYYH-QKYRGV-RNGIFWGTWPGVSEAHPGGYKSSFKE 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 VNNLLTMMSTSNSKDPTVAKEEQIS-----FRDCAEVFKSGHTTNGIYTLTFPNSTE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
Yu J., Han L.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Novel Human cDNA clones with function of inhibiting cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 244 AA; 27825 MW; E9D0ACBF87A7139E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01.MAR.2001 (TrEMBirel. 16, Created)
01.MAR-2001 (TrEMBirel. 16, Last sequence update)
01.DEC-2001 (TrEMBirel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 244 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002181; Fibrinogen_C.
Pfam; PF00147; fibrinogen_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical 27.8 kDa protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF218015; AAG17257.1; -. HSSP; P02671; 1FZD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00186; FBG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   483 VOMMIKP 489
                                                                                                                                                                                                                                                                                                                                                                                                            428 AKMMIRP 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09HBP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
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120 KTEMVQLQQSAVHNHTAAML-----EMGTSLLSQTAEQTRKLTDVETQVLNQTSRLEI 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 ------KLLSSELKNAKEEINVLH---GRLE------KLNLVNMNNIENYVDS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 QLLENSLSTNKLEKQLMIQINEINKIHDKNGFLEEKMOELEDRHRQELESLRTEKSDLQA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 LVSRQSSVIRELENQLSRATGNSTALQRQQQDLMESMRSLLSLCAKDAATAVEPNSTKQA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 TRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 QKTWKEYKMGFGSVSGEHWLGNEFVHVLINDRQHGLRVELSDWDGHQAFSQYDSFHIDSE 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 FLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDAC 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 DGNTCREFKSGTAYNANALQRDAPQPEADLSNQKIQQLEHVMENYTQWLQKIENYIKDNM 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 QDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN------RVRELESEV----- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 ----YKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNF 264 ::||:||:||:||:||::||::|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 DEERKFRDCADLYQAGFQKNGVYTINISPQETK-KVYCVMESAGGGWTVIQKREDGTVDF 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 127; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----SRIEEVFKE-VONLKEIVNSLKKSC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 WLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCE---EAGECPYQVSLPPL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 WWGCLFLA--ALLVVADCGGVEQKTDGLWSSTPKSNSSSGRRYHRIQHGQCSYTFILPES 59
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE-21391693; PubMed=11500985;
Pham V.N., Roman B.L., Weinstein B.M.;
"Isolation and expression analysis of three zebrafish angiopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385 LSANLNGKYYHQ-KYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          467 GPSNLNGVYYRQGQHVGKFNGIKWHYFKGPS-----YSLRSTVMMIRGADF 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.7%; Score 491.5; DB 13; Length 513; 26.6%; Pred. No. 2.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; ĀF379602; AAK83347.1; -.
InterPro: IPR002181; Fibrinogen_C.
Pfam; PF00147, fibrinogen_C; 1.
PRUTS; PR01609; BAIDNASINC.
PROSITE: PS00514; FIBRIN AG_C_DOMAIN; UNKNOWN_1.
SEQUENCE 513 AA; 58360 MW; 0627777739847D8B CRC64;
                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86; Mismatches 179;
                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Zebra danio).
                                                                                                                                                        513 AA.
                                                                                                                                                      PRT;
416 AHPGGYKSSFKEAKMMIRPKHF 437
                                            228 ---SGY--SLKATTMMIRPADF 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dyn. 221:470-474(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 TIQLPKQF------
                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                       Angiopoletin-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                          Q90Z19
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                                         Пр
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Search completed: December 2, 2002, 06:53:23 Job time : 122.903 secs

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December 2, 2002, 06:38:29; Search time 61.8855 Seconds (without alignments) 945.247 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS2/gcgdata/geneseg/genesegp-embl/AA1999.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA2000.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseg/genesegp-embl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS2/gcgdata/geneseg/genesegp-embl/AA1985.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1986.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1980.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   908470 segs, 133250620 residues
                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                          US-09-902-563-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             imum DB seq length: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                             Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/SIDS2/gcgdata/geneseg/genesegp-embl/AA2002.DAT:*

		Description	Human prothrombina	Mouse prothrombina	Rat hepatic parenc	Human TIE-2 ligand	Human TIE-2 ligand	Human TIE-2 ligand	Human angiopoietin	Human anglopoletin	Human anglopoletin	Amino acid sequenc
	í,	1D	-	AAW88236	AAR65759	AAW01411	AAR94605	AAW47532	AAB28392	AAY78903	AAY78906	AAU77944
	5	; : :	20	20	15	17	17	19	21	21	21	23
	4 4 0	rengun	439	432	314	496	496	496	496	496	496	496
d	Query	Match	100.0	77.9	22.0	22.0	22.0	22.0	22.0	22.0	22.0	22.0
	04000	arone	2378	1853.5	524	522	522	522	522	522	522	522
	Result		1	7	Э	4	2	9	7	œ	σ	10

19-NOV-1998.

human di human di acid seq angiopoi acid seq in encode	Human cancer assoc Hepatcoyte prolife Human TEE ligand N Anglopoletin-like Human PRO188 prote Amino acid sequenc An anglopoietin-re Human RRO188 polyp Human pRO188 polyp Human neovasculari Human angloponesis	TIE 119 hepatic secrete -FD-Fc-F AR-1 pr TIE 119 angiopo PRO356	prot CDT6 immu PRO3 PRO3 angi
ABG06771 ABG11614 AAW47528 AAU77252 AAW47529 AAR48000	AAAB4363 AAY26136 AAY26136 AAAY05397 AAB4739 AAY69483 AAY68761 AAY68761 AAB60340	AAE19826 AAR65760 AAX44811 AAX195780 AAX23736 AAX05399 AAX90400 AAX9408 AAB33432 AAB33432 AAB33432	76811634
22 12 13 17 17	22 22 22 22 22 22 23	211222123221232	1222222
V E Q 4 Q Q L L	4 4 9 9 1 1 2 2 3 4 4 4 9 9 1 2 2 3 4 4 9 9 1 1 4 9 9 1 1 1 1	010844444	4444448
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NANANANA	222222222222222222222222222222222222222		KKKKKKK
522 521.5 521.5 520 517.5 506.5	50 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	500 500 500 500 500 600 600 600 600 600	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
11 12 14 15 17 10	119 22 23 24 25 27	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	5 4 4 4 4 4 4 4 3 (S

ALIGNMENTS

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Prothrombinase; hfg12; Fg12; human; immune coagulation; antibody; inhibitor; infection; graft rejection; glomerulonephritis; cancer; gastrointestinal disease; foetal loss; therapy; vaccine.
                                                                                                                                                                                                                                                                                                       /note= "fibrinogen related domain"
364..378
                                                                                                                                                                                                                               /note= "Asn is N-glycosylated"
262..265
                                                                                                                                                                                                                                                           /note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                /note= "Asn is N-glycosylated"
213..439
                                                                                                                                                                                                          /label= Asn is N-glycosylated 235..238
                                                                                                                                                                                                                                                                                                                                /note= "epitope (Claim 4)"
                    AAW88235 standard; Protein; 439 AA.
                                                                                                                                                                                      Location/Qualifiers
                                                                                          Human prothrombinase Fgl2 protein.
                                                                 15-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                      ..337
                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                      WO9851335-A1.
                                            AAW88235;
                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                              Domain
RESULT 1
           AAW88235
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Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                    Domain
     AAW88236
                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LPPLTIQLFKQFSRIEBUFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYALGKRSSETYRVTPDPKNSSFEV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 APGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 YCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMIL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 KDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVRNGIFWGTWPGVSEAHPGG 420
                                                                                                                                                                                                                                                                                                         predicted from hfgl2 DNA (see AAV84139). Fgl2 is a 70 kba transmembrane serine protease that has immune procoagulant activity. The invention provides a method for inhibiting immune coagulation by inhibiting the activity or expression of Fgl2. The method can be used in vivo to treat a condition which requires a reduction in immune coagulation such as bacterial and viral infections, cancer,
                                                                                                                                                                                                                                                                                                                                                                                                           glomerulonephritis, a number of gastrointestinal diseases, allograft and xenograft rejection and foetal loss. An Fg12-specific antibody, an Fg12 antisense oligonucleotide, or a substance that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLANWYWLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYOVS 60
                                                                                                                                                                                          Modulating immune coagulation - by using Fgl2 antibodies and compounds, used to treat conditions including graft rejection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                           affects prothrombinase activity of a Fg12 protein may be used to treat a condition requiring a reduction in procoagulant activity. A vaccine containing an Fg12 protein or peptide is used for prevention of graft rejection or foetal loss (claimed).
                                                                                                                                                                                                                                                                                        This is the amino acid sequence of human prothrombinase Fg12, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 2378; DB 20; Length 439; Best Local Similarity 100.0%; Pred. No. 1.9e-205; Matches 439; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                               Claim 8; Page 66-67; 105pp; English.
98WO-CA00475.
                                               97US-0046537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 YKSSFKEAKMMIRPKHFKP 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 YKSSFKEAKMMIRPKHFKP 439
                                 97US-0061684,
                                                                                                                                            WPI; 1999-059687/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439 AA;
                                                                                                                                                               N-PSDB; AAV84139
                                                                               (LEVY/) LEVY G.
15-MAY-1998;
                                               15-MAY-1997;
                               10-OCT-1997;
                                                                                                                                                                                                                               foetal loss
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90 90 90 do Q Qy Db

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Db Oy DP Qy

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allograft and xenograft rejection and foetal loss. An Fg12-specific antibody, an Fg12 antisense oligonucleotide, or a substance that
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                                                                                                                                                                                                                                                                                     inhibitor; infection; graft rejection; glomerulonephritis; cancer; gastrointestinal disease; foetal loss; therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used to treat conditions including graft rejection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          affects prothrombinase activity of a Fg12 protein may be used to treat a condition requiring a reduction in procoagulant activity. A vaccine containing an Fg12 protein or peptide is used for prevention of graft rejection or foetal loss (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.9%; Score 1853.5; DB 20; Length 432; 77.7%; Pred. No. 3.4e-158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modulating immune coagulation - by using Fg12 antibodies and
                                                                                                                                                                                                                                                      Prothrombinase; Fg12; mouse; immune coagulation; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "fibrinogen related domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Asn is N-glycosylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page 70-71; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
AAW88236 standard; Protein; 432 AA.
                                                                                                                                                                                            Mouse prothrombinase Fg12 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0046537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-CA00475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0061684
                                                                                                                           15-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 341; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256..259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228..231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-059687/05.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV84140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LEVY/) LEVY G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9851335-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-0CT-1997;
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                                                                 AAW88236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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1 MKLANWYWLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVS 60

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(HPGF). The protein or the N-terminal peptide (AAR65758) may be used in the diagnosis and treatment of liver diseases, such as liver cancer and
                                                                                                                            22.0%; Score 524; DB 15; Length 314; 37.6%; Pred. No. 1.4e-38; tive 46; Mismatches 104; Indels 56; Gaps
                                                                                                                                                                                                                                                                                                                                                                                             231 HQTMKFSTRDRDNDNY-NGNCAEEQSGWWFNRCHSANLNGYYYQGPYRAETDNGVVWYT 289
                                                                                                                                                                                                          125 VGD-NRVRE---LESEVNKLSSELKNAKEEI-NVLHGRLEKLNLVNMNNIENYVDSKVAN 179
                                                                                                                                                                                                                                                                                         180 LTFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFE 239
                                                                                                                                                                                                                                                                                                                              76 -----LGGK-----RH--YADCSEIYNDGFKHSGFYKIKPLQSLAEFS 111
                                                                                                                                                                                                                                                                                                                                                                       240 VYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNL---RREFWLGNDKIHLLTKSK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 EMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNCTAGDALRFNKH-----YN 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 HDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRG-VRNGIFWGT 409
                                                                                                                                                                                                                                       31 LGDENCLQEQVRLRAQVRQLETRVKQQQVVIAQLLHEK--EVQFLDRGQEDSFID---- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIE-2 ligand 2; tyrosine kinase with Ig and EGF homology domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor; antagonist; neovascularisation; wound healing; ischae
leukopaenia; thrombocytopaenia; anaemia; angiogenesis; tumour;
atherosclerosis; inflammation; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIE-2 agonists and antagonists and related DNA - useful for promoting or blocking neovascularisation, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aldrich TH, Bruno J, Davis S, Goldfarb M, Jone
Maisonpierre PC, Radziejewski C, Yancopoulos GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 WPGVSEAHPGGYKSSFKEAKMMIRPKHFKP 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 W------RGWWYSLKSVVMKIRPSDFIP 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW01411 standard; Protein; 496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Fig 6; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REGE-) REGENERON PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US04806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95WO-US12935.
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                                                                                                                                                                     124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human TIE-2 ligand 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-465021/46.
                                                                                                                                               Similarity
                                                                                       314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT44321
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                                               cirrhosis.
                                                                                         Sequence
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                                                                                                                                Query Match
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                                                                                     121 APGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANL 180
                                                                                                                                                                                                                       181 TFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYALGKRSSETYRVTPDPKNSSFEV 240
                                                                                                                                                                                                                                                                                                      241 YCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMIL 300
                                                                                                                                                                                                                                                                                                                              301 RIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPD 360
                                                                                                                                                                                                                                                                                                                                                                                                          361 KDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVRNGIFWGTWPGVSEAHPGG 420
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AAQ77818 encodes AAR65759 rat hepatic parenchymal cell growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatic parenchymal cell growth promoter peptide - is isolated from human or animal liver cell or produced by recombinant techniques and used for therapy of liver diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatic parenchymal cell growth factor; HPGF; liver diseases;
liver cancer; cirrhosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 YKSSFKEAKMMIRPKHFKP 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 YKSSFKQAKMMIRPKNFKP 432
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Query Match 22.0%; Score 522; DB 17; Length 496; Best Local Similarity 27.9%; Pred. No. 4.4e-38; Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 LKE-----IVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN---- 128
            Human TIE-2 (tyrosine kinase with Ig and EGF homology domains) ligand 2 (AAW01411) is a ligand that binds the TIE-2 receptor. Its amino acid sequence was deduced from a cDNA clone (AAT44321) derived from human foetal lung cells. TIE-2 ligand 2 is a receptor antagonist useful for blocking blood vessel growth, for tumour therapy and for treating a proliferative disorder of a blood-forming organ. It can be obtd. from natural sources or expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 IMENNTQWLMKLENYIQDNMKKEMVEIQQNAVQN------QTAVMIEIGTNLLNQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 -----RVRELESEV----LEKL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 TAEQTRKLTDVEAQVLNQTTRLELQLLEHSLSTNKLEKQILDQTSEINKLQDKNSFLEKK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 NLV------- NMNNIENYVDSKVANLTF------V 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
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                                                                                                                                                                                                                                                                                                                                                                    43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVFKEVQN 84
                                                                                                                                                                                                                                                                                                                                                                                                              26 MDSIGKKQYQVQHGSCSYTFILPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLEN 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human TIE-2 ligand 2 derived from pBluescript KS clone.
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                                                                                                                                                                                in transformed host cells.
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                                                                                                                                                                                                                                Sequence 496 AA;
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AAR94605 is a human TIE-2 (hTIE-2) ligand 2 derived from a pBluescript KS clone. hTIE-2 ligand DNAs of the invention are recombinant versions of the native ligand coding sequences and may be used to produce the ligands at a high yield. Antibodies and receptor bodies that bind to TIE-2 ligands may be used to inhibit ampiogenesis and neovascularisation (e.g. associated with tumour development) and the TIE-2 ligands themselves are useful to promote neovascularisation and wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 MDSIGKKOYQVQHGSCSYTFLLPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLEN 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g. for treatment of ischaemia. TIE-2 ligands are also useful to treat thromboembolytic disease, atherosclerosis. Inflammation and diabetes. Ligand bodies contg. TIE-2 ligands may also be useful for the delivery and targeting of growth factors, toxins etc. to sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding TIE-2 ligand and related vectors - useful in diagnosis and treatment of neovascularisation, tumours, etc., or to \,
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                                                                                                                                                                                                                                                                                                         Joidiarb M, Jones PF;
Yancopoulos GD;
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                                                                                                                                                                                                                                                                                                         Goldfarb M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     where their presence is advantageous.
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Maisonpierre PC, Radziejewski C,
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                                             95WO-US12935.
                                                                                           95US-0418595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promote wound healing, etc.
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Matches 138; Conserv
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                                             06-OCT-1995;
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18-APR-1996.
                                                                                                                                                                                    09-DEC-1994;
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Disclosure; Page 283-285; 298pp; English.
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162 NLV---
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43 LESRGKCE---EAGECPYQVSLPPL------TIQ--LPKQFSRIEEVFKEVQN 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified human TIE-2 receptor ligand(s) - useful for promoting wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used in the method of the invention, involving the production of TIE-2 ligands which promote healing. The nucleic acids, vectors and host cells used in the method of the invention are useful for the recombinant production of the ligands. The ligands, etc. are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric TIE ligand 2N1C1F; TIE-2 ligand; neovascularisation;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Human TIE-2 ligand 2 from clone pBluescript KS.
                                                                                                                                                                                                                                                                AAW47532 standard; Protein; 496 AA.
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Matches 138; Conservative
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02-AUG-1996;
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receptor VEGFRI. The present sequence is human angiopoietin-2. Angiopoietin-2 may be operatively attached to the anti-VEGF antibodies of the present invention. Angiopoietin-2 acts to disturb capillary structure and is thought to lead to vessel recgression. The anti-VEGF antibodies of the present invention are useful for the treatment and diagnosis of
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                                                                                                                                                                                                           184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD 243
                                                                                                                                                                                                                                                                                                                                                                                                                            244 METMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRID 303
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                                                                                                        195 VLAMEDKHIIQLQSIKEEKDQLQVLVSKQNSIIEELEKKIVTATVNNSVLQKQQHDLMET 254
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                        Query Match 22.0%; Score 522; DB 21; Length 496; Best Local Similarity 27.9%; Pred. No. 4.4e-38; Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps
                                                                                                                                                  86 IMENNTQWLMKLENYIQDNMKKEMVEIQQNAVQN------QTAVMIEIGTNLLNQ 134
                                                                                                                                                                              129 -----RVRELESEV-----LEKL 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVFKEVQN 84
                                                                                                  26 MDSIGKKOYOVQHGSCSYTFLLPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLEN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Angiopoietin-2; Ang-2; vascular endothelial growth factor; tumour; vascularisation; anglogenesis; blood vessel maturation; malignant; benign; binding ligand; cancer; aminophospholipid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human angiopoietin-2 amino acid sequence.
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 496 AA;
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counteracts the blood vessel maturally occurring angiogenesis antagonist when counteracts the blood vessel maturation and stability mediated by Ang-1.

Constabilisation factor, converting angiogenesis agonist, and is a maturation or stabilisation factor, converting immature vessels to mature vessels.

Con stabilisation factor, converting immature vessels to mature vessels.

Both Ang-1 and Ang-2 are useful in a therapeutic approach to the creatment of vascularised tumours. The invention relates to a binding ligand comprising a targeting agent that binds to a mainophospholipid, inked to a therapeutic agent (e.g. Ang-2). Aminophospholipids are stable consisting mature or causes tumour necrosis (possibly by cell- or complement-mediated cytotoxicity and/or apoptosis). The binding ligand induces cogulation (thrombosis) in tumour vessels. The binding ligand induces cogulation (thrombosis) in tumour complement-mediated cytotoxicity and/or apoptosis). The binding ligands are used to treat vascularised tumours, malignant or benign, in animals, especially large tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 22.0%; Score 522; DB 21; Length 496; Best Local Similarity 27.9%; Pred. No. 4.4e-38; Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 LKE----IVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN---- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 -----RVRELESEV-----LEKL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 TAEQTRKLTDVEAQVLNQTTRLELQLLEHSLSTNKLEKQILDQTSEINKLQDKNSFLEKK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 NLV------V TE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 VLAMEDKHIIQLQSIKEEKDQLQVLVSKQNSIIEELEKKIVTATVNNSVLQKQQHDLMET 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 METMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRID 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
                                                                                                                                                                                                                                                                                                                                                                This sequence represents the human angiopoietin-2 (Ang-2) amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 MDSIGKKQYQVQHGSCSYTFLLPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLEN 85
                                                                                      Binding ligand for aminophospholipid used in the treatment of vascularised tumours, comprises targeting component and therapeutic % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                               Disclosure; Page 257-259; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78906 standard; Protein; 496 AA.
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N-PSDB; AAZ92213.
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sequence. Ang-2 is a naturally occurring anglogenesis antegonist when vascular endothelial growth factor (VEGT) levels are low, and generally counteracts the blood vessel maturation and stability mediated by Ang-1.

Ang-1 is a naturally occurring anglogenesis agonist, and is a maturation or stabilisation factor, converting immature vessels to mature vessels.

Both Ang-1 and Ang-2 are useful in a therapeutic approach to the treatment of vascularised tumours. The invention relates to a composition comprising an anti-anihophospholipid antihody, or its antigen binding region. The composition is used to kill tumour vasculature endothelial cells. Aminophospholipids are stable and specific markers accessible on the luminal surface of tumour blood vessels. Any of or an Ang-2 may be used in the composition of the invention. The composition is used to treat malignant or benign vascularised tumours in animals, especially large
                                                                                                                                                unconjugated anti-aminophospholipid antibody; tumour blood vessel marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New composition for killing tumour vascular endothelial cells for treating solid tumours, comprises unconjugated anti-aminophospholipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.0%; Score 522; DB 21; Length 496; 27.9%; Pred. No. 4.4e-38; tive 74; Mismatches 159; Indels 124; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 VLAMEDKHIIQLQSIKEEKDQLQVLVSKQNSIIEELEKKIVTATVNNSVLOKOOHDLMET 254
                                                                                                                      Human; angiopoietin-2; Ang-2; aminophospholipid; vascularised tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the human angiopoietin-2 (Ang-2) amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 LESRGKCE---EAGECPYQVSLPPL------TIQ--LPKQFSRIEEVFKEVQN 84
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                                                         Human angiopoietin-2 (Ang-2) amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 223-224; 226pp; English.
                                                                                                                                                                            cancer; treatment; angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US15600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0110608.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98HS-0092672
19-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TEXA ) UNIV TEXAS SYSTEM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-182175/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ran S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAZ92215
                                                                                                                                                                                                                                                                                                WO200002584 - A2
                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                         20-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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anti-vege antibody; monoclonal antibody 2c3 ATCC PTA 1595; Veger receptor; Vegersk; KDR/FRLY, VeGRRI; FIL-1; andjodenesis; macular degeneration; ocular neovascular disease; cancer; vascularised solid tumour; ATDS; metastatic tumour; endothelial cell proliferation; inflammatory disorder; athersoclerosis; diabetic retinopathy; corneal graft rejection; acquired immune deficiency syndrome; infection; restenosis; fungal ulcer; sickle cell anaemia; endometriosis; anglopoietin-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immunoconjugate; anti-vascular endothelial growth factor antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to antibody-based compositions comprising an immunoconjugate such as anti-vascular endothelial growth factor (VEGP) antibody (Abb) (or its antigen-binding fragment), attached to a biological agent, where the Ab binds to the same epitope as the monoclonal antibody (MAb) 2C3 ARCC PTA 1595, and significantly inhibits VEGF binding to the VEGF receptor VEGFR2 (KDR/FIK-1) without inhibiting vEGF binding to the VEGF receptor VEGFR2 (FIL-1). The compositions of the invention are useful in therapy, and diagnosis, for inhibiting angiogenesis in an animal having ocular neovascular disease or macular degeneration, and for delivering a biological agent to a vascularised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprises
                                                                                                                                                                    364 DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
                                                                                                                                                                                                                                                                          431 DKCIC-KCSQMLTGGWWFDACGPSNLNGMYYPQRQNTNKFNGIKWYYWKG-----SGY- 482
255 VNNLLTMMSTSNSAKDPTVAKEEQISFRDCAEVFKSGHTTNGIYTLTFPNSTEEIKAYCD 314
                                               244 METMGGGWTVLQARLDGSTNFTRTWQDYRAGFGNLRREFWLGNDKIHLLLTKSKEMILRID 303
                                                                                         315 MEAGGGGWTIIQRREDGSVDFQRTWKEYKVGFGNPSGEYWLGNEFVSQLTNQQRYVLKIH 374
                                                                                                                                      304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDN 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoconjugate compositions for treating cancer by inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          angiogenesis and for delivering a diagnostic agent to tumour, anti-vascular endothelial growth factor antibody attached to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 4-6 (Sequence listing); 300pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence for human angiopoietin-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU77944 standard; Protein; 496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-2001; 2001AU-0079401.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-APR-2000; 2000AU-0048049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                         423 SSFKEAKMMIRPKHF 437
                                                                                                                                                                                                                                                                                                                                                                   483 -SLKATTMMIRPADF 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thorpe PE, Brekken RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-281368/33.
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tumour. The compositions can also be used for treating cancer and subjects at risk of developing, a vascularised solid tumour, a metastastic tumour or metastases from a primary tumour. The composition is useful for specifically inhibiting VEGF-induced endothelial cell proliferation, without significantly inhibiting VEGF-induced marcophage, osteoclast or chondroclast function. The compositions can be used for treating various alisases such as inflammatory disorders, atherosclerosis, diabetic retinopathy, restenosis, acquired immune deficiency syndrome (AIDS). Blood borne tumours, corneal graft rejection, Crohn's disease, fungal ulcers, infections, sickle cell anaemia, and endometriosis. The present sequence represents human angiopoletin-2. Angiopoletin-2 may be attached or functionally associated with anti-VEGF antibodies.
                                                                                                                                                                                                                                                                                                                       22.0%; Score 522; DB 23; Length 496; 27.9%; Pred. No. 4.4e-38; Live 74; Mismatches 159; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 LKE-----IVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN---- 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 METMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRID 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDN 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375 LKDWEGNEAYSLYEHFYLSSEELNYRIHLKGLTGTAGKISSISQPGND----FSTKDGDN 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
                                                                                                                                                                                                                                                                                                                                                                                                           43 LESRGKCE---EAGECPYQVSLPPL------TIQ--LPKQFSRIEEVFKEVQN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 MDSIGKKOYQVQHGSCSYTFLLPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLEN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #6762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG06771 standard; Protein; 572 AA.
                                                                                                                                                                                                                                                                                                                                                                Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                   496 AA;
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                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                           Query Match
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         8.5.6.6.6.6.6.6.6.6.6.5.5.5.5
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABGO010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.0%; Score 522; DB 22; Length 572;
27.9%; Pred. No. 5.6e-38;
Live 74; Mismatches 159; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 MDSIGKKQYQVQHGSCSYTFLLPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLEN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 LKE-----IVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN---- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 -----RVRELESEV-----LEKL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 TAEQTRKLIDVEAQVLNOTTRLELQLLEHSLSTNKLEKQILDQTSEINKLQDKNSFLEKK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 NLV-------V 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 VLAMEDKHIIQLQSIKEEKDQLQVLVSKQNSIIEELEKKIVTATVNNSVLQKQQHDLMET 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 METMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRID 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVFKEVQN 84
                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID No 37130; 103pp; English.
                                                                                                                                                                                                      Tang YT;
                                           30-MAR-2001; 2001WO-US08631.
                                                                                                                23-AUG-2000; 2000US-0649167.
                                                                                        31-MAR-2000; 2000US-0540217
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Best Local Similarity
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                                                                                                                                                         (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                   biodiversity
  11-OCT-2001,
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDN 363
                                          451 LKDWEGNEAYSLYEHFYLSSEELNYRIHLKGLTGTAGKISSISQPGND----FSTKDGDN 506
                                                                                        364 DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
                                                                                                                 to produce other types of data and products dependent on DNA and no acid sequences. ABG00010-ABG30377 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid sequences. ABG00010-ABG30377 represent diagnostic amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human diagnostic protein #11605
                                                                                                                                                                                                                                                                                                                                               ABG11614 standard; Protein; 1033 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-2002 (first entry)
                                                                                                                                                                                     423 SSFKEAKMMIRPKHF 437
                                                                                                                                                                                                                                559 -SLKATTMMIRPADF 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73.
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                                                                                                                                                                                                                                                                                                    RESULT 12
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Query Match 22.0%; Score 522; DB 22; Length 1033;
Best Local Similarity 27.9%; Pred. No. 1.4e-37;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps
                                                                                                                                   563 MDSIGKKQYQVQHGSCSYTFLLPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLEN 622
                                                                                                                                                                       85 LKE-----IVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN---- 128
                                                                                                                                                                                                                                                                         672 TAEQTRKLIDVEAQVLNQTTRLELQLLEHSLSTNKLEKQILDQTSEINKLQDKNSFLEKK 731
                                                                                                                                                                                                                                                                                                                                                                                                    304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDN 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
                                                                                                    43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVFKEVQN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of chimeric TIE ligand 1N1C2F (chimera 1).
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                                                                                                                                                                                                                                                                                                             ---NMNNIENYVDSKVANLTF-
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1033 AA;
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 Sequence
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tumour; human.
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                                                                                                                                                                                                                                                                                                 Seguence
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                                                                                                     used in the method of the invoition, involving the production of TIE-2 ligands which promote healing. The nucleic acids, vectors and host cells used in the method of the invention are useful for the recombinant production of the ligands. The ligands, etc. are useful for blocking blood vessel growth, promoting neovascularisation, promoting the growth or differentiation of a cell expressing the TIE receptor, blocking the growth or differentiation of a cell expressing the TIE receptor and for attenuating or preventing tumour growth in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 NRATTNN--SVLQXQQLELMDTVHNLVNLCTREGVLLKGGKREEEKP-----FRDCAEVF 290
                                                                                                                                                                                                                                                                                                                                                                         61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                       113 GLLLPSTGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHG------RLEK-L 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 SLL------EHKILEME---GKHKEELDTLKEEKENLQGLVTRQTYIIQELEKQL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 NLVNMNNIENYVDSKVANLIFVVNSLDGKCSK----CPSQEQIQSRPVQHLIYKDCSDYY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 AIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGN 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 KSGHTTNGIYTLTFPNSTEEIKAYCDMEAGGGGWTIIQRREDGSVDFQRTWKEYKVGFGN 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 PSGEYWLGNEFVSQLTNQORYVLKIHLKDWEGNEAYSLYEDFYLSSEELNYRIHLKGLTG 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411 TAGKISSISQPGND----FSTKDGDNDKCIC-KCSQMLTGGWWFDACGPSNLNGMYYPQR 465
                                                                                                                                                                                                                                                                                                                                           71; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       145 LTDVETQVLNQTSRLEIQLLENSLSTYKLEKQLLQQTNEILKIHE------KN 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 LRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  338 TAGDALRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQK 397
            Modified human TIE-2 receptor ligand(s) - useful for promoting wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; angiopoletin-2-443; Ang2_443; Tie-2 receptor-related disorder.
                                                                                             This is the amino acid sequence of the chimeric TIE ligand INIC2F,
                                                                                                                                                                                                                                                                                                        21.9%; Score 521.5; DB 19; Length 498; 32.7%; Pred. No. 5e-38; tive 61; Mismatches 138; Indels 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 398 YRGVR-NGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 466 QNTNKFNGIKWYYWKG----SGY--SLKATTMMIRPADF 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU77252 standard; Protein; 444 AA.
                                                           Claim 20; Fig 24; 202pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human anglopoietin-2-443 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-OCT-2000; 2000KR-0060202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-OCT-1999; 99KR-0044605.
                                                                                                                                                                                                                                                                                                                                        Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                          498 AA;
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                                                                                                                                                                                                                                                                            Seguence
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                               healing
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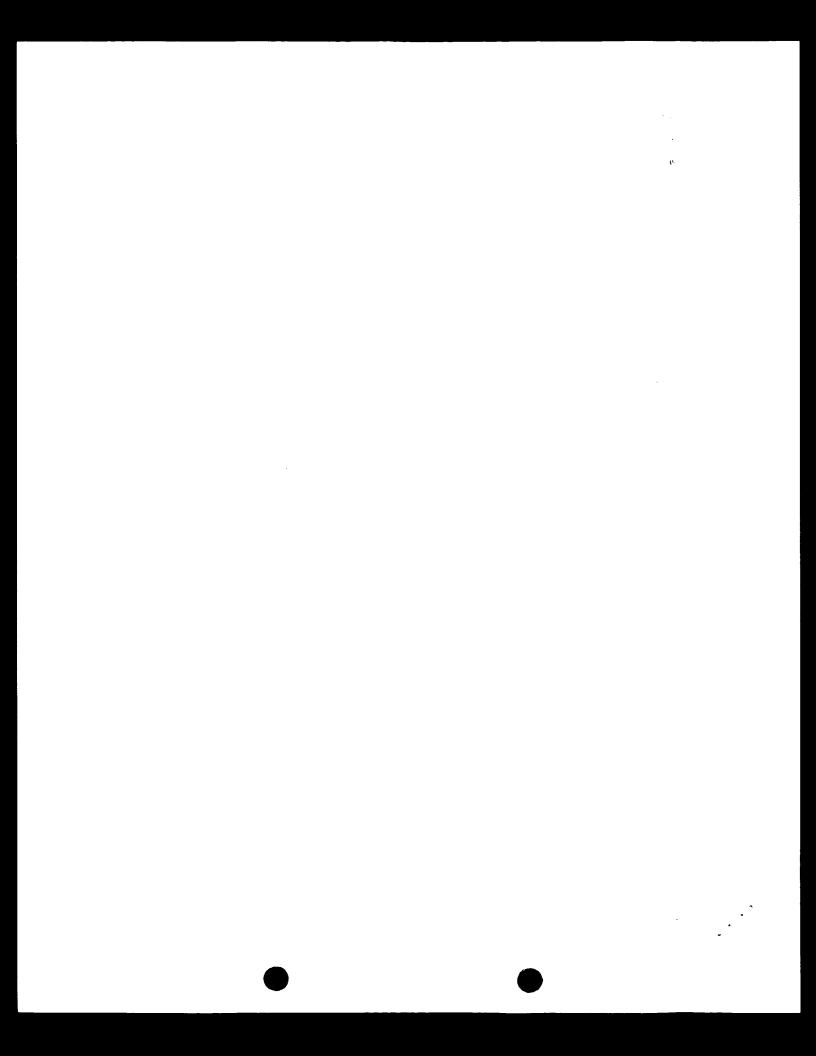
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15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the isolation of human angiopoietin-2-443 (Ang2_443) protein and the gene encoding it. The sequences of the invention can be used in the prevention and treatment of diseases related to cells which express the Tie-2 receptor. The present sequence represents human Ang2_443 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 21.9%; Score 520; DB 23; Length 444;
Local Similarity 29.6%; Pred. No. 5.7e-38;
nes 134; Conservative 74; Mismatches 154; Indels 90; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 SLKKSC-----QDCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVRELESEVNKLSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 IMENNTQWLMKVLNQTTRLELQ-----LLEHSLSTNKL-EKQILDQTSEINKLQD 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 ------ELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVAN---- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 ------LIFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSET 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 KOOHDLMETVNNLLTMMSTSNSAKDPTVAKEEQIS-----FRDCAEVFKSGHTTNGI 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 YRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGN 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 DKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 KHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGI 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366 QPGND----FSTKDGDNDKCIC-KCSQMLTGGWWFDACGPSNLNGMYYPQRQNTNKFNGI 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 KNSFLEKKVLAMEDKHIIQLQSIKEEKDQLQVLVSKQNSI-IEELEKKIVTATVNNSVLQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 LESRGKCE---EAGECPYQVSLPPL----TIQLPKQFSRIE-----EVFKEVQNLKEIVN 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 MDSIGKKQYQVQHGSCSYTFLLPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLEN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of chimeric TIE ligand 1N2C2F (chimera 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric TIE ligand 1N2C2F; TIE-2 ligand; neovascularisation;
                                                                                                                                                                                                                                                                                          Human angiopoietin-2-443 protein and its gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             406 FWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW47529 standard; Protein; 499 AA.
                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 12; 17pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 134; Conservative
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(BIOR-) BIOROUTE CO LID.
                                                                                                                                                                 WPI; 2002-065267/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 444 AA;
                                                                                                                                                                                                    N-PSDB; ABK10923
                                                                                Ko GY;
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12-FEB-1998

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\begin{tabular}{ll} Modified $human\ TIE-2$ receptor ligand(s) - useful for promoting wound healing $healing$ $healing $healing$ $healing $healing$ $heali
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                                                                                                                                                                                                                                                                                                                                       (REGE-) REGENERON PHARM INC.
                                                                                                                         97WO-US13557
                                                                                                                                                                                                                                                        960S-0022999.
                                                                                                                                                                                                             96US-0740223
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N-PSDB; AAV18616.
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                                                                                                                         01-AUG-1997;
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02-AUG-1996;
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Search completed: December 2, 2002, 06:50:27 Job time: 64.8855 secs

used in the method of the invention, involving the production of TIE-2 ligands which promote healing. The nucleic acids, vectors and host cells used in the method of the invention are useful for the recombinant production of the ligands. The ligands, etc. are useful for blocking blood vessel growth, promoting neovascularisation, promoting the growth or differentiation of a cell expressing the TIE receptor, blocking the growth or differentiation of a cell expressing the TIE receptor and for attenuating or preventing tumour growth in 160 ELQLLEHSLSTNKLEKQILDQTSEINKLQDKNSFLEKKVLAMEDKHIIQLQSIKEEKDQL 219 165 ----NMNNIENYVDSKVANLTF-----VVNSLDGKCSKCPSQEQIQSRPV 205 206 QHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFT 265 326 LKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACL 385 Ouery Match 21.8%; Score 517.5; DB 19; Length 499; Best Local Similarity 28.1%; Pred. No. 1.1e-37; Matches 133; Conservative 73; Mismatches 166; Indels 101; Gaps 49 EHDGNCRESTIDQYNTNALQRDAPHVEPDDSVQRLQVLENIME -- NNTQWLMKLENYIQD 106 95 SCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN------RVRELESEV---- 137 107 NMKKEMVEIQQNAVQNQTAVMI-----EIGTNLLNQTAEQTRKLTDVEAQVLNQTTRL 159 220 QVLVSKQNSIIEELEKKIVTATVNNSVLQKQQHDLMETVNNLLIMMSTSNSAKDPTVAKE 279 266 RTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEF 325 138 ----- NKLSSELKNAKEEINVLHGR---LEKLNLV------- 164 44 ESRGKCEEAGECPYQVSL------PPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKK 94 This is the amino acid sequence of the chimeric TIE ligand IN2C2F, 386 SANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437



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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

December 2, 2002, 06:53:36; Search time 13.5374 Seconds Run on:

(without alignments) 516.399 Million cell updates/sec

US-09-902-563-2 2378 Title: Perfect score:

1 MKLANWYWLSSAVLATYGFL......GYKSSFKEAKMMIRPKHFKP 439 Sednence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

tal number of hits satisfying chosen parameters:

102317 seqs, 15924203 residues

Searched:

Inimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: (cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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7: (cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: (cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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10: (cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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11: (cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:* /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.* /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.* /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.* Published_Applications_AA:* 10: 11: 12: 13:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 6, Appli	Sequence 4, Appli	Sequence 14, Appl	Sequence 1082, Ap	Sequence 1, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 13, Appl	Sequence 23, Appl	Seguence 2, Appli	Sequence 5, Appli	Seguence 1, Appli	Sequence 1, Appli	Sequence 314, App	Sequence 314, App	Sequence 314, App	314,	Sequence 314, App	Sequence 314, App
ID	US-10-179-744-6	US-09-998-831-4	US-09-897-306-14	US-09-925-301-1082	US-09-897-306-1	US-10-179-744-4	US-09-998-831-2	US-09-897-306-13	US-09-818-143-23	US-10-179-744-2	US-09-998-831-5	US-09-912-740A-1	US-09-912-741B-1	US-09-992-598-314	US-09-989-722-314	US-09-989-723-314	US-09-989-279-314	US-09-989-727-314	US-09-989-731-314
DB	6	10	10	10	10	S	10	10	10	σ	10	6	10	6	10	10	10	10	10
Query Match Length DB	496	496	496	339	491	497	498	498	493	498	495	411	411	461	461	461	461	461	461
Query Match	22.0	22.0	22.0	21.3	21.2	20.5	20.5	20.5	20.3	20.3	20.1	19.7	19.7	19.4	19.4	19.4	19.4	19.4	19.4
Score	522	522	522	206	505	487	486.5	486.5	480.5	480.5	478.5	468	468	460.5	460.5	460.5	460.5	460.5	460.5
Result No.	Н	7	3	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19

	Sequence 3, Appli Sequence 29, Appl
10 US-09-989-732-314 10 US-09-991-73-314 10 US-09-991-163-314 10 US-09-991-163-314 10 US-09-991-163-314 10 US-09-990-456-314 10 US-09-990-721-314 10 US-09-989-721-314 10 US-09-986-546-26 10 US-10-112-527-1 10 US-09-966-546-26 10 US-09-966-546-28 10 US-09-966-546-28 10 US-09-966-546-28 10 US-09-966-546-28 10 US-09-966-546-28 10 US-09-966-546-28 10 US-09-778-927A-61 10 US-09-966-546-185 10 US-09-989-920-185 10 US-09-989-920-185 10 US-09-989-920-185 10 US-09-989-920-185 10 US-09-989-920-185 10 US-09-989-920-185 10 US-09-989-989-888-1	9 US-US-888-5 10 US-09-939-825-29
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ALIGNMENTS

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184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD 243
                            244 METMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRID 303
                                                                                                                                                                 304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRENKHYNHDLKFFTTPDKDN 363
                                                                                                                                                                                                                                               364 DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 22.0%; Score 522; DB 10; Length 496; Best Local Similarity 27.9%; Pred. No. 7e-35; Marches 138; Conservative 74; Mismatches 159; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 IMENNTQWILMKLENYIQDNMKKEMVEIQQNAVQN------QTAVMIEIGTNLLNQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 NLV------V TRAINTENYVDSKVANLTF-----V 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDN 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 LKE----IVNSLKKSCQDCKLQADDNGDPGRNGLLPSTGAPGEVGDN---- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 -----RVRELESEV------LEKL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 TAEQTRKLIDVEAQVLNQTTRLELQLLEHSLSTNKLEKQILDQTSEINKLQDKNSFLEKK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 VLAMEDKHIIOLOSIKEEKDOLQVLVSKONSIIEELEKKIVTATVNNSVLQKQQHDLMET 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 VNNLLTMMSTSNSAKDPTVAKEEQISFRDCAEVFKSGHTTNGIYTLTFPNSTEEIKAYCD 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 METMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRID 303
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APPLICANT: ROLF A. Brekken
TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY
TITLE OF INVENTION: INHIBITING VEGF
FILLE REPERRING: 4001.002584
CURRENT APPLICATION NUMBER: US/09/998,831
CURRENT FILLING DATE: 2001-11-30
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PRIOR FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09998831
Patent No. US20020119153A1
GENERAL INFORMATION:
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Query Match 22.0%; Score 522; DB 10; Length 496; Best Local Similarity 27.9%; Pred. No. 7e-35; Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;
364 DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
                              85 LKE-----IVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN---- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 IMENNTQWLMKLENYIQDNMKKEMVEIQQNAVQN------QTAVMIELGTNLLNQ 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 NLV------- NMNNIENYVDSKVANLTF------V 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 METMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRID 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 LESRGKCE---EAGECPYQVSLPPL------TIQ--LPKQFSRIEEVFKEVQN 84
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; OTHER INFORMATION: Incyte ID No. US20020123054A1 g2257933
US-09-897-306-14
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APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN ANGIOPOLETIN
FILE REFERENCE: PC-0048 CIP
CURRENT APPLICATION NUMBER: US/09/897,306
                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09897306
Patent No. US20020123054A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-07-02
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                                                                                                                  423 SSFKEAKMMIRPKHF 437
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SOFTWARE: PERL Program
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; Sequence 4, Application US/10179744
; Patent No. US20020173627A1
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327 KYRLHVGNYNGTAGDALRFNKH-----YNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWW 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381 FDACLSANLNGKYYHQKYRG-VRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHFKP 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 DYKAGFGNL---RREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANFFL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 DYENGFGNFVORHGEYWLGNKNLHFLTTQEDYTLKIDLADFEKNSRYAQYKNFKVGDEKN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 FYELNIGEYSGTAGDSLAGNFHPEVQWWASHQRMKFSTWDRDHDNY-EGNCAEEDQSGWW 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.3%; Score 506; DB 10; Length 339; 44.6%; Pred. No. 8.3e-34; tive 25; Mismatches 88; Indels 2
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                                                                                                                                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
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CURRENT APPLICATION NUMBER: US/09/897,306
CURRENT FILING DATE: 2001-07-02
NUMBER OF SEO ID NOS: 14
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/925,301 CURRENT FILING DATE: 2001-08-10 PRIOR APPLICATION NUMBER: PCT/US00/05882 PRIOR FILING DATE: 2000-03-08
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APPLICANT: Patterson, Chandra
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN ANGIOPOLETIN
                                                                                                                            Sequence 1082, Application US/09925301 Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/124,270
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Patent No. US20020123054A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 1694
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SOFTWARE: PatentIn Ver. 2.0
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483 -SLKATTMMIRPADF 496
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                                                                                                                                                                             GENERAL INFORMATION:
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Query Match 21.2%; Score 505; DB 10; Length 491; Best Local Similarity 26.9%; Pred. No. 1.7e-33; Matches 131; Conservative 81; Mismatches 137; Indels 138; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRN 112
                                                                                                                                                                                                 98 DCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGR 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 ------IYKDCSDYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGG 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 GWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 VELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYPSG 369
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                                                                                                                                               47 GKCEEAGECPYQVSLPPLTIQLP------KQFSRIEEVF--KEVQNLKEIVNSLKKSCQ 97
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Unknown Organism US-10-179-744-4
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192 SLL------BHKILBME---GKHKEELDTLKEEKENLQGLVTRQTYIIQELEKQL 237
                                                                 162 NLVNMNNIENYVDSKVANLTFVVNSLDGKCSK---CPSQEQIQSRPVQHLIYKDCSDYYA 218
                                                                                                                     238 NRATTNN--SVLOKOQLELMDTVHNLVNLCTKEVLLKGGKREEDKP-----FRDCADVYQ 290
                                                                                                                                                                                                    291 AGFNKSGIYTIYINNMPEPK----KVFCNMDVNGGGWTVIQHREDGSLDFQRGWKEYKMG 346
                                                                                                                                                                                                                                                              275 FGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGN 334
                                                                                                                                                                     219 IGKRSSETYRV----TPDDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAG 274
                                                                                                                                                                                                                                                                                                               347 FGNPSGEYWLGNEFIFAITSQRQYMLRIELMDWEGNRAYSQYDRFHIGNEKQNYRLYLKG 406
                                                                                                                                                                                                                                                                                                                                                                                                           407 HTGTAGKQSSLILH-GAD---FSTKDADNDNCMC-KCALMLTGGWWFDACGPSNLNGMFY 461
                                                                                                                                                                                                                                                                                                                                                               335 YNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYY 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LPPLTIQLPKQFSRIE-----BVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 LTDVETQVLNQTSRLEIQLLENSLSTYKLEKQLLQQTNEILKIHE------KN 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 GFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVG 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INCOMMUTION:
APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
TITLE OF INVENTION: INHIBITING VEGF
TITLE OF INVENTION: INHIBITING VEGF
FILE REFERENCE: 4001.002584
CURRENT APPLICATION NUMBER: US/09/998,831
CURRENT FILING DATE: 2001-11-30
PRIOR PLILNG DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.5%; Score 486.5; DB 10; Length 498; 32.3%; Pred. No. 5.4e-32; tive 59; Mismatches 136; Indels 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             395 HQ-KYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462 TAGONHGKINGIKWHYFKGPS-----YSLRSTTMMIRPLDF 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09998831
Patent No. US20020119153A1
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SOFTWARE: Patentin Ver. 2.0
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79; Gaps 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRN 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020123054A1 g1907327
US-09-897-306-13
                                   394 YHQ-KYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437
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CURRENT FILING DATE: 2001-07-02
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gorgone, Gina A.
APPLICANT: Patterson, Chandra
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN ANGIOPOLETIN
FILE REFERENCE: PC-0048 CIP
                                                                                                                                                                                                           Sequence 13, Application US/09897306
; Patent No. US20020123054A1
; GENERAL INFORMATION:
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; Patent No. US20020019000A1
                                                                                                                                                                                                                                                                                                  APPLICANT: Hillman, Jennifer L.
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Ouery Match 20.2%; Score 480.5; DB 10; Length 493; Best Local Similarity 30.8%; Pred. No. 1.6e-31; Matches 117; Conservative 62; Mismatches 128; Indels 73; Gaps 12;
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Best Local Similarity 32.1%; Pred. No. 1.7e-31;
Matches 130; Conservative 59; Mismatches 137; Indels 79; Gaps 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 -----TSLPSSTDKPSGP-----WRDCLQALEDGHDTSSIYLVKPENTNRL 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 PGEVGD----NRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 PPRVYQPPTYNRI;-----INQISTNEIQSDQNLKVLPPPLLPTMPTL------261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 ANLTFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSS 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Davis, Samuel et al.
TITLE OF INVENTION: TIEL ELIGANIS, METHODS OF MAKING AND USES THEREOF
FILE REPERANCE: REG 310-2 LIGANIS,
CURRENT APPLICATION NUMBER: US/10/179,744
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: US/08/817,318
PRIOR FILING DATE: 1999-09-16
CURRENT APPLICATION NUMBER: US/09/818,143
CURRENT FILINS DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 6 SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10179744
Patent No. US20020173627A1
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US-09-818-143-23
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                                                                                                                                                                                               ORGANISM: Homo sapiens
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                                                                                                                                           493
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US-10-179-744-2
                                                                                                                  SEQ ID NO 23
                                                                                                                                                                     TYPE: PRT
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Oy dq	113	GLLLPSTGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEK-L 161
oy Oy	162	NMNNIENYVDSKVANLTEVANSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYY 2
Db	238	:: : : :: : NRATTNNSVLQKQQLELMDTVHNLVNLCTKEGVLLKGGKREEERPFRDCADVY 290
Qy Dp	218	AIGKRSSETYRVTPDPKNSSFEVYCDMETWGGGWTVLQARLDGSTNFTRFWQDYKA 273
δy	274	33
Dp	347	40
QY	334	NYNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKY 393 :
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	uence ent l FPAT	Sequence 5, Application US/US98831 Patent No. US2002019153A1 CENTEDAT INCORMATAN.
	PLIC!	INVERMATION: NT: Philip E. Thorpe NT: Rolf A Brekken
	TE	TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY TITLE OF INVENTION: INHIBITING VEGF
	RRENT RRENT	FERENCE: 4001.002304 APPLICATION NUMBER: US/09/998,831 FILING DATE: 2001-11-30
	PRIOR PRIOR I	APPLICATION NUMBER: 09/561,108 FILING DATE: 2000-04-28
u	MBEF FTWP	SEQ ID NC PatentIn
U I	ENGI	Δ.
; ORGAN ; ORGAN US-09-998	11FE: FRI ORGANISM: 9-998-831	rri 1881: Homo sapiens -831-5
Que	ry Ma	Query Match 20.1%; Score 478.5; DB 10; Length 495;
Mat	ches	vative 58; Mismatches
δλ	61	LPPITIQLPRQFSRIEEVFKEVQNLKEIVNSLKRSCQDCKLQADDNGDPGRN 112
qq	142	LTDVETQVLNQTSRLEIQLEENSLSTYKLEKQLLQQTNEILKIHEKN 188
Qy	113	GLLLPSTGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEK-L 161
QQ	189	SLLEHKILEMEGKHKEELDTLKEEKENLQGLVTRQTYIIQELEKQL 234
Qy	162	NLVNMNNIENYDSKVANLTEVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSD 215
qq	235	NRATTNNSVLQKQQLELMDTVHNLVNLSTKEGVLLKGGKREEEKPFRDCAD 285
Qy	216	YYAIGKRSSETYRVTPDPRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDY 271
Db.	286	KVFCNMDVNGGWTVIQHREDGSLDFQRGWK
 δÿ	272	KAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLH 331
Db	342	KMGFGNPSGEYWLGNEFIFAITSQRQYMLRIELMDWEGNRAYSQYDRFHIGNEKQNYRLY 401

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NAME/KEY: CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Unknown
                                                                                                                                                                                                                                                                           US-09-912-741B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-912-741B-1
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                                                                                                                               qq
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                                                                                                                                                                                                                                                332 VGNYNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Mismatches 168; Indels 64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 VQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVRELESEVNKLS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 VENKTSEVKOLIKA----IQLTYNPDESSKPNMIDAATLKSRIMLEEIMKYEASILTHD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 SELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANLTFVVNSLDGKCSKCPSQEQIQ 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 SSIRYLQE-----IYNSNN-----QKIVNLKEKVAQLEAQCQE-PCKDTVQ 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 SRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 ---IHDITGKDCQDIANKGAKQSGLYFIKPLKANQQFLVYCEIDGSGNGWIVFQKRLDGS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VATRDNCCILDERFGSYCPT-----TCGIADFLSTYQTKVDKDLQSLEDILHQ 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 VANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVSLPPLTIQLPKQFSRIEEVFKE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 19.7%; Score 468; DB 9; Length 411; Best Local Similarity 30.6%; Pred. No. 1.3e-30;
                                                                      392 KYYHQ-KYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437
                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: site of glycosylation
                                                                                                                                                                                                 ; Sequence 1, Application US/09912740A
; Patent No. US20020169280A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (153)...(182)
OTHER INFORMATION: disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ...CATION: (326)...(339); OTHER INFORMATION: disulfide-bond US-09-912-740A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 126; Conservative
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                                                                                                                                                                RESULT 12
US-09-912-740A-1
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APPLICANT: Languino, Lucia R
APPLICANT: Thornton, George B
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
TITLE OF INVENTION: BUDOTHELIAL CELL AND FIBRINOGEN MEDIATED INFLAMMATION
FILE REPERRORE: 300-101v4
CURRENT APPLICATION NUMBER: US/09/912,741B
PRIOR APPLICATION NUMBER: US/09/347,877
PRIOR FILING DATE: 1999-07-06
PRIOR APPLICATION NUMBER: US 08/748,150
262 TNFTRTWQDYKAGFGNL----RREFWLGNDKIHLLTKSKEM--ILRIDLEDFNGVELYAL, 315
                                    202 VDFKKNWIQYKEGFGHLSPTGTTEFWLGNEKIHLISTQSAIPYALRVELEDWNGRTSTAD 261
                                                                                                                               316 YDQFYVANEFLKYRLHVGNY-NGTAGDAL-RFNKHYNHDLKFFT-----TPDKDNDR 365
                                                                                                                                                                                                    262 YAMFKVGPEADKYRLTYAYFAGGDAGDAFDGFDFGDDPSDKFFTSHNGMQFSTWDNDNDK 321
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                                                                                                                                                                                                                                                                  366 YPSGNCGLYYSSGWWFDACLSANLNGKYYH-----QKYRGVRNGIFWGTW 410
                                                                                                                                                                                                                                                                                                      54; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1996-11-12
PRIOR APPLICATION NUMBER: US 08/232,532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1993-10-19
PRIOR APPLICATION NUMBER: US 07/898,117
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OTHER INFORMATION: disulfide-bond
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OTHER INFORMATION: disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1994-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1992-06-12
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Matches 126; Conserva
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316 YDQFYVANEFLKYRLHVGNY-NGTAGDAL-RFNKHYNHDLKFFT-----TPDKDNDR 365
...
105 SSIRYLQE-----IYNSNN-----QKIVNLKEKVAQLEAQCQE-PCKDTVQ 144
                                                      202 SRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGS 261
                                                                                                                                       262 TNFTRTWQDYKAGFGNL----RREFWLGNDKIHLLTKSKEM--ILRIDLEDFNGVELYAL 315
                                                                                                                                                             145 ---IHDITGKDCQDIANKGAKQSGLYFIKPLKANQQFLVYCEIDGSGNGWIVFQKRLDGS 201
                                                                                                                                                                                                                                                                                                      366 YPSGNCGLYYSSGWWFDACLSANLNGKYYH-----QKYRGVRNGIFWGTW 410
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bequence 314, Application US/09992598 Patent No. US20020160384A1 SULT 14 -09-992-598-314

APPLICANT: Ashkenazi, Avi J. GENERAL INFORMATION:

Baker, Kevin P. Botstein, David Desnoyers, Luc APPLICANT: APPLICANT APPLICANT

Ferrara, Napoleone Gerber, Hanspeter Fong, Sherman Eaton, Dan L. APPLICANT:

Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J. APPLICANT:

Grimaldi, J. Christopher Gurney, Austin L. Kljavin, Ivar J. Napier, Mary A. Pan,James

Paoni, Nicholas F.

APPLICANT:

Watanabe, Colin K. Williams, P. Mickey Wood, William I. Timothy A. Roy, Margaret Ann Daniel Stewart, APPLICANT: APPLICANT: APPLICANT:

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same Acids Encoding the Same APPLICANT: APPLICANT

FILE REFERENCE: P2730P1C20 CURRENT APPLICATION NUMBER: US/09/992,598 CURRENT FILING DATE: 2001-11-14 PRIOR APPLICATION NUMBER: 60/049787

PRIOR APPLICATION NUMBER: 60/062250 FILING DATE: 1997-06-16 PRIOR

PRIOR APPLICATION UNMBER: 00/002230
PRIOR PLING DAFE: 1997-10-17
PRIOR PLING DAFE: 1997-110-17
PRIOR FILING DAFE: 1997-11-12
PRIOR PLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/06731
PRIOR PLING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/0670
PRIOR PLING DATE: 1998-12-25
PRIOR PLICATION NUMBER: 60/078910
PRIOR PLICATION NUMBER: 60/078910
PRIOR PLILING DATE: 1998-03-26
PRIOR PLILING DATE: 1998-04-28
PRIOR PLILING DATE: 1998-05-07
PRIOR PLILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07

FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088876 FILING DATE: 1998-06-11 FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/089440 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089538 FILING DATE: 1998-06-17 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089599 PRIOR FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/088030 FILLING DATE: 1998-06-04 APPLICATION NUMBER: 60/088033 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088167 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088824 FILING DATE: 1998-06-10 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088861 APPLICATION NUMBER: 60/089105 APPLICATION NUMBER: 60/089514 APPLICATION NUMBER: 60/089532 APPLICATION NUMBER: 60/089598 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087609 PRIOR APPLICATION NUMBER: 60/087759 PRIOR FILING DATE: 1998-06-02 PRIOR APPLICATION NUMBER: 60/087827 PRIOR FILING DATE: 1998-06-03 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088029 FILING DATE: 1998-06-04 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088326 APPLICATION NUMBER: 60/088202 APPLICATION NUMBER: 60/088212 APPLICATION NUMBER: 60/088217 APPLICATION NUMBER: 60/088655 APPLICATION NUMBER: 60/088734 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088738 APPLICATION NUMBER: 60/088742 APPLICATION NUMBER: 60/088858 APPLICATION NUMBER: 60/088025 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088026 APPLICATION NUMBER: 60/088028 APPLICATION NUMBER: 60/087607 APPLICATION NUMBER: 60/088021 FILING DATE: 1998-06-05 FILING DATE: 1998-06-10 FILING DATE: 1998-06-05 FILING DATE: 1998-06-09 FILING DATE: 1998-06-16 FILING DATE: 1998-06-05 FILING DATE: 1998-06-17 1998-06-02 FILING DATE: 1998-06-04 FILING DATE: 1998-06-04 1998-06-1 FILING DATE: 1998-06-1 FILING DATE: PRIOR PRIOR

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241 P-----RDCLDVLLSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVN 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 FSVDPEEDGYPLTVADYSGTAGDSL----LKHSGMRFTTKDRDSD-HSENNCAAFYRGA 408
                                                                                                                                                                                                                                        57 YQVSLPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLL 116
                                                                                                                                                                                                                                                                               90 LSILIDPRCPDLTDSFARLE-----LT 120
                                                                                                                                                                                                                                                                                                                           117 PSTGAPGEVGDNRVRELESEVNKL-----SSELKNAKEEINVLHGRL------EKL 161
                                                                                                                                                                                                                                                                                                                                                                     121 EHQAQPRLVGDQEQELLDTLADQLPRLLARASELQTECMGLRKGHGTLGQGLSALQSEQG 180
                                                                                                                                                                                                                                                                                                                                                                                                               162 NLVN-MNNIENYVDSKVANLTFVVNSL--DGKCSKCPSQEQIQ------SR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 PVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTN 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 FTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVA- 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zhang, Zemin
TILLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                    7 YWLSSAVLATYGFLVVA-NNETEEIKDERAKDVCPVRLESRGKC------EEAGECP 56
                                                                                                                                                                                            30 YVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGTAPPPVVSTGAASANSALVTVERADSSH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379 WWFDACLSANLNGKYYHQKYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRP 434
                                                                 Ouery Match 19.4%; Score 460.5; DB 9; Length 461; Best Local Similarity 28.8%; Pred. No. 6.4e-30; Matches 137; Conservative 60; Mismatches 182; Indels 97,
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CURRENT APPLICATION NUMBER: US/09/989,722
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Williams, P. Mickey
Wood, William I.
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Gerritsen, Mary E.
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Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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US-09-989-722-314
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PRIOR APPLICATION NUMBER: 60/08792
PRIOR FILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-03
PRIOR PELICATION NUMBER: 60/08021
PRIOR PELICATION NUMBER: 60/08021
PRIOR APPLICATION NUMBER: 60/08025
PRIOR PELICATION NUMBER: 60/08026
PRIOR PILING DATE: 1998-06-04
PRIOR PELICATION NUMBER: 60/08026
PRIOR PILING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-11
PRIOR PILING DATE: 1998-06-11 PRIOR FILING DATE: 1998-02-25 PRIOR APPLICATION NUMBER: 60/078910 PRIOR FILING DATE: 1998-03-20 PRIOR APPLICATION NUMBER: 60/087609 PRIOR FILING DATE: 1998-06-02 PRIOR APPLICATION NUMBER: 60/062250 PRIOR FILING DATE: 1997-10-17 PRIOR FILING DATE: 1997-11-13 PRIOR APPLICATION NUMBER: 60/066770 PRIOR FILING DATE: 1997-11-24 PRIOR APPLICATION NUMBER: 60/087106 PRIOR APPLICATION NUMBER: 60/049787 PRIOR FILING DATE: 1997-06-16 PRIOR APPLICATION NUMBER: 60/083322 PRIOR APPLICATION NUMBER: 60/084600 PRIOR APPLICATION NUMBER: 60/087759 PRIOR APPLICATION NUMBER: 60/065186 PRIOR FILING DATE: 1997-11-12 PRIOR APPLICATION NUMBER: 60/065311 PRIOR APPLICATION NUMBER: 60/075945 PRIOR APPLICATION NUMBER: 60/087607 CURRENT FILING DATE: 2001-11-19 1998-04-28 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-28 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE:

FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-24 PRIOR APPLICATION NUMBER: 60/090676 PRIOR FILING DATE: 1998-06-25 PRIOR FILING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/090690 PRIOR APPLICATION NUMBER: 60/090695 PRIOR FILING DATE: 1998-06-25 PRIOR FILING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/090696 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090435 APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090445 PRIOR APPLICATION NUMBER: 60/090557 PRIOR FILING DATE: 1998-06-24 PRIOR APPLICATION NUMBER: 60/090678 APPLICATION NUMBER: 60/090694 FILING DATE: 1998-06-25 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089908 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090246 APPLICATION NUMBER: 60/090252 APPLICATION NUMBER: 60/090355 APPLICATION NUMBER: 60/090431 APPLICATION NUMBER: 60/089440 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089538 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089599 APPLICATION NUMBER: 60/089600 APPLICATION NUMBER: 60/089947 APPLICATION NUMBER: 60/089105 FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/089512 APPLICATION NUMBER: 60/089532 APPLICATION NUMBER: 60/089801 APPLICATION NUMBER: 60/089514 APPLICATION NUMBER: 60/089598 PRIOR FILING DATE: 1998-06-25 FILING DATE: 1998-06-18 FILING DATE: 1998-06-18 FILING DATE: 1998-06-19 FILING DATE: 1998-06-24 FILING DATE: 1998-06-16 FILING DATE: 1998-06-16 FILING DATE: 1998-06-16 FILING DATE: 1998-06-17 FILING DATE: 1998-06-1 FILING DATE: 1998-06-2 FILING DATE: 1998-06-1 PRIOR PRIOR

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19.4%; Score 460.5; DB 10; Length 461; 28.8%; Pred. No. 6.4e-30; tive 60; Mismatches 182; Indels 97; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 NLVN-MNNIENYVDSKVANLTFVVNSL--DGKCSKCPSQEQIQ------SR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 YQVSLPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 LSILIDPRCPDLTDSFARLE------LT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 PSTGAPGEVGDNRVRELESEVNKL----SSELKNAKEEINVLHGRL------EKL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 PVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTN 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 P-----RDCLDVLLSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVN 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 FTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVA- 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 ----NEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 FSVDPEEDGYPLTVADYSGTAGDSL----LKHSGMRFTTKDRDSD-HSENNCAAFYRGA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 YWLSSAVLATYGFLVVA-NNETEE1KDERAKDVCPVRLESRGKC------EEAGECP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 YVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGTAPPPVVSTGAASANSALVTVERADSSH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  379 WWFDACLSANLNGKYYHQKYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRP 434
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091860
PRIOR APPLICATION NUMBER: 60/091478
PRIOR PLICATION NUMBER: 60/091478
PRIOR APPLICATION NUMBER: 60/091544
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-02
PRIOR PELICATION NUMBER: 60/09154
PRIOR PLILNG DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091635
PRIOR PLILNG DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091637
PRIOR APPLICATION NUMBER: 60/091637
PRIOR APPLICATION NUMBER: 60/091637
PRIOR PLILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
                                                       FILING DATE: 1998-06-26
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Best Local Similarity 28.8%
Matches 137; Conservative
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Search completed: December 2, 2002, 07:00:06 Job time: 14.5374 secs

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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: December 2, 2002, 06:49:20; Search time 26.1079 Seconds
(without alignments)
494.741 Million cell updates/sec
Title: US-09-902-563-2
Perfect score: 2378
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Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 262574 seqs, 29422922 residues
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tal number of hits satisfying chosen parameters: 2625

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ď			SUMMARIES		
Result No.	Score	Query Match	Length DB	DB	ID	Description	
1	2378	100.0	439	4	IIS-09-442-143A-2	Ι.	Appli
	1853 5	77 9			-00-442	ì -	1.PP.1.1
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4	524	22.0	496	1 4	US-09-202-491-7	į [-	Appli
5	522	22.0		4	-08-740-223	α	Appli
9	522	22.0		4	-09-709-1	8	Appli
7	522	22.0	4	Н	US-08-373-579-6	9	Appli
æ	522	22.0	4	7	US-08-418-595-6	9	Appli
6	522	22.0	4	7	US-08-665-926-6	9	Appli
10	522	22.0	4	4	US-09-162-437-6	9	Appli
11	522	22.0	4	4	US-08-740-223A-6	9	Appli
12	522	22.0	4	4	US-09-351-457-4	4	Appli
13	522	22.0	4	4	US-09-561-500-4	4,	Appli
14	522	22.0	496	4		4	Appli
15	522	22.0	4	4	US-09-351-543-4	4,	Appli
16	522	22.0	4	4	US-09-561-526-4	4	Appli
17	522	22.0	4	4	US-09-202-491-8	8	ppli
18	522	22.0	4	4	-08-817-318-	9	Appli
19	522	22.0	4	4	US-09-709-188-6	9	Appli
20	2	21.9	4	4	US-08-740-223A-20	20,	Appl
21	521.5	21.9	4	4	US-09-709-188-20	20,	Appl
22	\vdash	21.8	4	4	US-08-740-223A-24	24,	Appl
23	517.5	21.8	4	4	US-09-709-188-24	24,	App1
24	510	21.4	4	4	US-08-740-223A-15	15,	Appl
25	510	21.4	4	4	US-09-709-188-15	15,	Appl
26	506.5	21.3	(.4	٣	-08-960-201-	20,	Appl
27	506.5	21.3	286	4	US-09-136-801-20	20,	Appl

Sequence 4, Appli	4,	Sequence 4, Appli	Sequence 4, Appl	Sequence 4, Appl	Sequence 4, Appl	Sequence 16, App	Sequence 16, App	Sequence 19, App.	Sequence 19, App.	Sequence 4, Appl	Sequence 4, Appl	Sequence 12, App.	Sequence 12, App.	Sequence 22, App	Sequence 22, App	Sequence 4, Appl
US-08-525-505A-4 US-08-933-821-4	US-08-960-507-4	US-09-136-828-4	US-09-332-928A-4	US-09-136-801-4	US-09-332-929-4	US-08-740-223A-16	US-09-709-188-16	US-08-960-507-19	US-09-136-801-19	US-08-740-223A-4	US-09-709-188-4	US-08-740-223A-12	US-09-709-188-12	US-08-740-223A-22	US-09-709-188-22	US-08-373-579-4
7	m	4	4	4	4	4	4	3	4	4	4	4	4	4	4	-
312	491	491	491	491	491	496	496	346	346	497	497	490	490	496	496	497
21.3	21.2	21.2	21.2	21.2	21.2	20.9	20.9	20.6	20.6	20.5	20.5	20.5	20.5	20.5	20.5	20.5
506	505	505	505	502	505	498	498	489	489	488	488	487	487	487	487	487
28	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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61 LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 APGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TEVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 YCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMIL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 YCDMETMGGGWTVLQARLDGSTNFTRTWQDYRAGFGNLRREFWLGNDKIHLLTKSKEMIL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 RIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPD 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 2378; DB 4; Length 439; Best Local Similarity 100.0%; Pred. No. 5.8e-211; Matches 439; Conservative 0; Mismatches 0; Indels 0;
                                                                                                 APPLICANT: Levy, Gary
APPLICANT: Clark, David A.
IIILE OF INVENTION: Methods of Modulating Immune Coagulation
FILE REFERENCE: 9579-14
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/442,143A CURRENT FILING DATE: 1999-11-15
                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/046,537 PRIOR FILING DATE: 1997-05-17 PRIOR APPLICATION NUMBER: US 60/061,684
                 ; Sequence 2, Application US/09442143A; Patent No. 6403089
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1997-10-10
NUMBER OF SEQ ID NOS: 53
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                                                                             ; GENERAL INFORMATION:
US-09-442-143A-2
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                361 KDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVRGIFWGTWPGVSEAHPGG 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEV 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.9%; Score 1853.5; DB 4; Length 432; 77.7%; Pred. No. 1.3e-162; tive 42; Mismatches 49; Indels 7;
                                                                                                                                                                                                                                                               APPLICANT: Levy, Gary
APPLICANT: Clark David A.
TITLE OF INVENTION: Methods of Modulating Immune Coagulation
FILE REFERENCE: 9579-14
CURRENT APPLICATION NUMBER: US/09/442,143A
CURRENT FILING DATE: 1999-11-15
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/046,537 PRIOR FILING DATE: 1997-05-17 PRIOR APPLICATION NUMBER: US 60/061,684 PRIOR FILING DATE: 1997-10-10 NUMBER OF SEQ ID NOS: 53 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                        ; Sequence 4, Application US/09442143A
; Patent No. 6403089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/08525505A
                                                                         421 YKSSFKEAKMMIRPKHFKP 439
                                                                                              421 YKSSFKEAKMMIRPKHFKP 439
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Matches 341; Conservative
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                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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125 VGD-NRVRE---LESEVNKLSSELKNAKEEI-NVLHGRLEKLNLVNMNNIENYVDSKVAN 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 ------LGGK-------RH--YADCSEIYNDGFKHSGFYKIKPLQSLAEFS 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 EMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKH-----YN 350
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                                                                                                           APPLICANT: SHINDO, SAEKO
APPLICANT: HANADA, KAZUNORI
TITLE OF INVENTION: PARENCHYMAL HEPTOCYTE GROWTH SUBSTANCE
NUMBER OF SEGEDENESS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.0%; Score 524; DB 1; Length 314; 37.6%; Pred. No. 3e-40; tive 46; Mismatches 104; Indels
                                                                                                                                                                                                                      OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                  : 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/525,505A FILING DATE: 22-SEP-1995
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FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                       APPLICANT: HARA, HIROSHI
APPLICANT: YOSHIMURA, HIROMITSU
APPLICANT: MATSUKI, YUMIKO
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 22-MAR-1994
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: P
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MEDIUM TYPE: Floppy of
                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                         USA
Patent No. 5807711
                                                                                                                                                                                                                             ADDRESSEE:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 LOKQOHDLMETVNSLLTMMSSPNSKSSVAIRKEEQTTFRDCAEIFKSGLTTSGIYTLTFP 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 TKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHD 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 LKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWP 411
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                                                                                                                                                                                                           APPLICANT: Valenzuela et al.
TITLE OF INVENTION: NOVEL LIGANDS, METHODS OF MAKING AND USES THEREOF
FILE REFERENCE: REG330-K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 22.0%; Score 524; DB 4; Length 496; Best Local Similarity 32.9%; Pred. No. 6e-40; Matches 127; Conservative 65; Mismatches 154; Indels 40;
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                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: PCI/US97/10728
                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/202,491
290 W-----RGWWYSLKSVVMKIRPSDFIP 311
                                                                                                                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1997-06-19
EARLIER APPLICATION NUMBER: 60/022,999
EARLIER FILING DATE: 1996-08-02
EARLIER FILING DATE: 1996-07-02
EARLIER FILING DATE: 1996-07-02
EARLIER FILING DATE: 1996-07-02
BARLIER FILING DATE: 1996-06-19
NUMBER OF SEG ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                            Sequence 7, Application US/09202491
Patent No. 6432667
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CORRESPONDENCE ADDRESS:
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                                                                                 RESULT 4
US-09-202-491-7
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Query Match 22.0%; Score 522; DB 4; Length 480;
Best Local Similarity 27.9%; Pred. No. 8.7e-40;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 -----RVRELESEV-----LEKL 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: USSN 60/022/999
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/740,223A FILING DATE: 25-OCT-1996
                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
STREET: 777 Old Saw Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Mature TL2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36,108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 914-345-7721 INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                            IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cobert, Robert J
                                                                                                                                                                                                                                            DOS
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            914-345-7721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1...480
OTHER INFORMATION:
                                                                                                                                                                                                                                   OPERATING SYSTEM:
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STRANDEDNESS: sir
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                                Tarrytown
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                                                                                          USA
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TOPOLOGY:
                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                    APPLICANT: Davis et al.
TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
FILE REFERENCE: REG 333.2
CURRENT APPLICATION NUMBER: US/09/709,188
CURRENT FILE NO DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 08/740,223
PRIOR PILING DATE: 1996-10-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 IMENNTQWLMKLENYIQDNMKKEMVEIQQNAVQN------QTAVMIEIGTNLLNQ 118
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APPLICANT: Davis, et al.
TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
                                                                                                                                                     ; Sequence 8, Application US/09709188
; Patent No. 6441137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-373-579-6; Sequence 6, Application US/08373579; Patent No. 5650490
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin version 3.1
SEQ_ID_NO 8
                                      467 -SLKATTMMIRPADF 480
423 SSFKEAKMMIRPKHF 437
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                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens US-09-709-188-8
                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 NLV-----
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                                                                                                                           US-09-709-188-8
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Query Match 22.0%; Score 522; DB 1; Length 496; Best Local Similarity 27.9%; Pred. No. 9.1e-40; Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVFKEVQN 84
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                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                 Regeneron Pharmaceuticals, Inc.
                                                                           ADDRESSEE: Regeneron Pharmaceutican:
STREET: 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
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APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-0CT-1994
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07-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/373,579 FILING DATE: 17-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JMBER: US 08/348,492
02-DEC-1994
                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Cobert, Robert J. REGISTRATION NUMBER: 36,108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (914) 345-7400
TELEPAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-OCT-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 496 amino acids
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                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER: (
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                             NUMBER OF SEQUENCES:
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                                                                                                                                   Tarrytown
                                                                                                                                                                STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                          USA
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304 LEDFINGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDN 363
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                                                  85 LKE-----IVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN--- 128
                                                                                               86 IMENNTQWIMKLENYIQDNMKKEMVEIQONAVON------QTAVMIEIGTNLINQ 134
                                                                                                                                                 -----NKLSSELKNAKEEINVLHGR---LEKL 161
                                                                                                                                                                                              135 TAEQTRKLTDVEAQVENQTTRLELQLLEHSLSTNKLEKQILDQTSEINKLQDKNSFLEKK 194
                                                                                                                                                                                                                                                 -------NMNNIENYVDSKVANLTF-----V 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 MEAGGGGWTIIQRREDGSVDFQRTWKEYKVGFGNPSGEYWLGNEFVSQLTNQQRYVLKIH 374
  26 MDSIGKKQYQVQHGSCSYTFLLPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLEN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.30
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REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/665,926 FILLING DATE: 19-JUN-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
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; Patent No. 5851797
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TELEPHONE: (914) 345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Valenzuela et al.
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                 129 -----RVRELESEV----
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                                                  375 LKDWEGNEAYSLYEHFYLSSEELNYRIHLKGLTGTAGKISSISQPGND ---FSTKDGDN 430
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27.9%; Pred. No. 9.1e-40;
tive 74; Mismatches 159; Indels 124; Gaps
304 LEDFINGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDN 363
                                                                                                    364 DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
                                                                                                                                                 431 DKCIC-KCSQMLTGGWWFDACGPSNLNGMYYPQRQNTNKFNGIKWYYWKG-----SGY- 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Davis, et al. TILE-2 LIGAND, METHOD OF MAKING AND USES TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: Regeneron Pharmaceuticals, Inc.: 777 Old Saw Mill River Road
Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-0CT-1994
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/373,579
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FILING DATE: 06-APR-1995
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08418595 Patent No. 5814464
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IBM PC compatible
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TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 6:
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ZIP: 10591
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Ouery Match 22.0%; Score 522; DB 2; Length 496; Best Local Similarity 27.9%; Pred. No. 9.1e-40; Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         ...----NMNNIENYVDSKVANLTF------V 183
                                                                                                                                                                                                                                  85 LKE-----IVNSLKKSCQDCKLQADDNGDPGRNGLLPSTGAPGEVGDN---- 128
                                                                                                                                                                                                                                                                                                                        129 -----RVRELESEV-----LEKL 161
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                                                                                                                                      43 LESRGKCE---EAGECPYQVSLPPL------TIQ--LPKQFSRIEEVFKEVQN 84
                                                                                                                                                                          26 MDSIGKKQYQVQHGSCSYTFLLPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLEN 85
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COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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. APPLICATION NUMBER: 08/418,595
.FILING DATE: 06-APR-1995
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APPLICANT: Davis, et al.
TITLE OF INVENTION: TIE-:
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US-08-665-926-6
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Query Match 22.0%; Score 522; DB 4; Length 496;
Best Local Similarity 27.9%; Pred. No. 9.1e-40;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps
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                                                                                                                               FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING APPLICATION NUMBER:
             APPLICATION NUMBER: US 08/353,503 FILING DATE: 09-DEC-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/348,492 FILING DATE: 02-DEC-1994
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Patent No. 6265564
GENFRAL
                                                                                                                                                                                                                               FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: CODERT, ROBERT 36,108
REGISTRATION NUMBER: 36,108
                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: RETELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 (914) 345-7400
FILING DATE: 17-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (914) 345-7721 INFORMATION FOR SEQ ID NO:
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amino acid
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; MOLECULE TYPE: protein
US-09-162-437-6
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                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: I
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184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD 243
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Best Local Similarity 27.9%; Pred. No. 9.1e-40;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 TAEQTRKLTDVEAQVLNQTTRLELQLLEHSLSTNKLEKQILDQTSEINKLQDKNSFLEKK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 NLV------ 183
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                                  Expressed Ligand - Vascular Intercellular Signalling Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: from clone pBluescript KS OTHER INFORMATION: encoding human TIE 2 ligand 2
                                                                                                                     ADDRESSEE: Regeneron Pharmaceuticals, Inc. STREET: 777 Old Saw Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/022/999
FLIING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/740,223A FILING DATE: 25-OCT-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REG 333
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                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                            : Diskette
IBM Compatible
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914-345-7721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           496 amino acids
APPLICANT: Davis, et al.
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                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                     TITLE OF INVENTION:
TITLE OF INVENTION:
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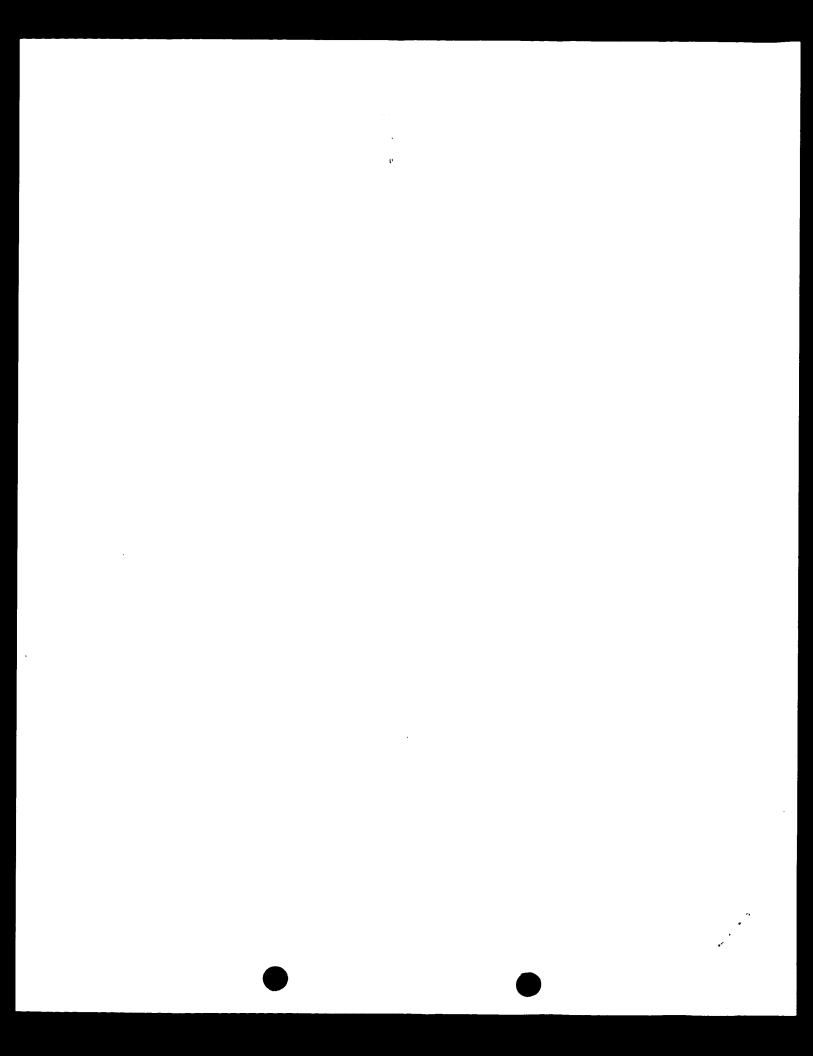
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APPLICANT: THORPE, PHILIP E. APPLICANT: THORPE, PHILIP E. APPLICANT: TRAN, SOPHIA TITLE OF INVENTION: CANCER TREATMENT METHODS USING THERAPEUTIC CONJUGATES TITLE OF INVENTION: THAT BIND TO AMINOPHOSPHOLIPIDS
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Best Local Similarity 27.9%; Pred. No. 9.1e-40;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps
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304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDN 363
                                                                                               375 LKDWEGNEAYSLYEHFYLSSEELNYRIHLKGLTGTAGKISSISQPGND----FSTKDGDN 430
                                                                                                                                                                                                          364 DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09351457 Patent No. 6312694
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CURRENT APPLICATION NUMBER: US/09/351,543
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 5
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; Patent No. 6406693
CURRENT FILING DATE: 2000-04-28
                 PRIOR APPLICATION NUMBER: 60/1
PRIOR FILING DATE: 1999-04-28
                                                                              SOFTWARE: Patentin Ver. 2.0
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                                                          NUMBER OF SEQ ID NOS: 44
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APPLICANT: ROLLE A. Brekken
TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002584
CURRENT APPLICATION NUMBER: US/09/561,108
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                                                                                                       APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002500
CURRENT APPLICATION NUMBER: US/09/561,500
CURRENT FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                               22.0%; Score 522; DB 4; Length 496; 27.9%; Pred. No. 9.1e-40; tive 74; Mismatches 159; Indels 124; Gaps
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PRIOR APPLICATION NUMBER: 60/131,432
PRIOR FILING DATE: 1999-04-28
                                            ; Sequence 4, Application US/09561500
; Patent No. 6342219
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Patent No. 6342221
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SOFTWARE: Patentin Ver. 2.0
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Ouery Match 22.0%; Score 522; DB 4; Length 496;
Best Local Similarity 27.9%; Pred. No. 9.1e-40;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps
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APPLICANT: THORPE, PHILIP E.
APPLICANT: RAN, SOPHIA
ITILE OF INVENTION: CANCER TREATMENT METHODS USING ANTIBODIES TO'
ITILE OF INVENTION: AMINOPHOSPHOLIPIDS
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Best cocal Similarity 27.9%; Pred. No. 9.1e-40;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;
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                                                                                                                                                                                                                                                                              43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVFKEVQN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423 SSFKEAKMMIRPKHF 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              483 -SLKATTMMIRPADF 496
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Search completed: December 2, 2002, 06:54:34 Job time: 28:1079 secs



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GenCore version 5.1.3
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OM protein - protein search, using sw model

December 2, 2002, 06:48:57; Search time 1.05727 Seconds (without alignments) 1363.907 Million cell updates/sec Run on:

US-09-902-563-18 Perfect score: Title:

1 DRYPSGNCGLYYSSG 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

tal number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* PIR 73:* Database :

pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	fibrinogen-like or		fibrinogen-like pr		reelin precursor -	hypothetical prote	Ψ				−w	hypothetical prote				Æ	gene P2 protein -	outer membrane pro	xylan 1,4-beta-xyl	ferredoxin - Therm	hypothetical 11.49	hypothetical prote	\vdash	actin-capping prot		~	e-tRN	early E2A DNA-bind	early E2A DNA-bind
	ID	I56934	A27447	137391	A59386	S58870	C82893	149707	T24007	C86624	H72000	G71829	T16246	A81289	T26404	A72513	ERADA7	WMBPQ2	H70347	T00131	A72242	JN0734	D86894	G64210	A33546	AF3043	F98242	E64454	ERAD41	ERAD12
	DB	5	7	7	7	7	7	7	7	7	7	7	7	7	~	7	-	-	7	7	7	7	~	7	7	~	7	7	Н	-
	Length	432	432	439	2403	3461	225	284	339	456	456	969	273	368	385	437	517	591	680	798	92	100	165	245	286	294	305	455	474	484
æ	Query Match	100.0	100.0	100.0	52.3	2	48.9	48.9	48.9	48.9	48.9		46.6		•	46.6					٠						45.5		•	45.5
	Score		88	88	46	46	43	43	43	43	43	42.5	41	41	41	41	41	41	41	41	40	40	40	40	40	40	40	40	40	40
	Result No.	1	7	3	4	2	9	_	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

L-2,4-diaminobutyr	hypothetical prote	androgen-requiated	zinc-finger protei	alpha,alpha-trehal	Ig heavy chain v r	ubiquitin/ribosoma	ubiquitin / riboso	ubiquitin extensio	ubiquitin extensio	ubiquitin / riboso	ubiquitin / riboso				
T44576	D87413	S28258	T18297	S54500	128195	S25001	JH0226	JH0227	JS0657	UQTO7A	S25305	T52334	T52335	D36571	C36571
7	7	~	7	7	7	7	7	7	7	-	7	7	7	7	~
490	521	176	1151	1211	117	118	155	155	155	156	156	156	156	157	157
5.5	45.5	45.5	45.5	45.5	44.3	44.3	44.3	44.3	44.3	44.3	44.3	44.3	44.3	44.3	44.3
4															
40 4		40	40	40	39	39	39	39	39	39	39	39	39	39	39

ALIGNMENTS

RESULT 1

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R.Parr, R.L.; Fung, L.; Reneker, J.; Myers-Mason, N.; Leibowitz, J.L.; Levy, G. J. Virol, 69, 5033-5038, 1995
A: Vittle: Association of mouse fibrinogen-like protein with murine hepatitis virus-ind A; Reference number: 156934; MUID:95333285; PMID:7609073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                               C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytotoxic T-lymphocyte-specific protein precursor (clone pT49) - mouse C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB:S78773; NID:g1042169; PIDN:AAB34823.1; PID:g1042170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology F;203-428/Domain: fibrinogen beta/gamma homology <FBG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 88; DB 2; Length 432; Best Local Similarity 100.0%; Pred. No. 2e-06; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-432 <RES>
fibrinogen-like protein - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357 DRYPSGNCGLYYSSG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DRYPSGNCGLYYSSG 15
                                                                                                          C;Accession: I56934
                                                                                                                                                                                                                                                                                                 A; Accession: I56934
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C;Accession: A27447

R;Koyama, T.; Hall, L.R.; Haser, W.G.; Tonegawa, S.; Saito, H.

Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987

A;Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology

A;Reference number: A27447; WUID:87175527; PMID:3550794

A; Molecule type: mRNA A; Residues: 1-432 <KOY>

A;Cross-references: GB:M16238; NID:g193304; PIDN:AAA37624.1; PID:g387156-C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology F;203-428/Domain: fibrinogen beta/gamma homology <FBG>

0; Gaps Query Match 100.0%; Score 88; DB 2; Length 432; Best Local Similarity 100.0%; Pred. No. 2e-06; Matches 15; Conservative 0; Mismatches 0; Indels

; 0

1 DRYPSGNCGLYYSSG 15

δy

Mon Dec 2 07:10:16 2002

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PEBS Lett. 355, 4-10, 1994

A:Title: Isolation and characterization of cDNA clones specifically expressed in test A; Reference number: 149707; MUID:95046372; PMID:7957958

A:Accession: 149707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE002139; GB:AF222894; NID:96899405; PIDN:AAF30837.1; GSPDB:GN
A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a A;Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÷
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                            A;Residues: 1-215,'T',217-1905,'S',1907-3355,'V',3357-3391,'N',3393-3461 cDa2>
A;Cross.references: EMBL:U24703; NID:g902486; PID:g902487
C;Superfamily: unassigned EGF-related proteins, EGF homology
E;1-27/Domain: signal sequence #status predicted <SIG>
F;28-3461/Product: reelin #status predicted <MAT>
F;18-3461/Product: EGF homology <EGF>
E;1769-1795/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein UU425 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: C82893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   germ cell specific gene 3 protein - mouse
C;Species: Mus musculus (house mouse)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 19-May-2000
C;Accession: 149707
                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                         Ouery Match 52.3%; Score 46; DB 2; Length 3461; Best Local Similarity 71.4%; Pred. No. 76; Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.9%; Score 43; DB 2; Length 225; 70.0%; Pred. No. 18; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.9%; Score 43; DB 2; Length 284;
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A.Cross-references: GB:D38545; NID:g603492; PID:g603493
C.Superfamily: actin-capping protein alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                1974 YPGGNIGLYCPYSS 1987
                                                                                                                                                                                                                                                                                                                                                                3 YPSGNCGLY--YSS 14
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   A; Molecule type: mRNA
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                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: Olvov-1996 fsequence_revision 01-Nov-1996 ftext_change 21-Jul-2000
C;Accession: 137391; S47273
R;Ruegg, C; Pytela, R.
Gene 160, 255-265, 1995
A;Title: Sequence of a human transcript expressed in T-lymphocytes and encoding a fibrir A;Reference number: 137391; MUID:95369700; PMID:7642106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:D'Arcangelo, G.; Miao, G.G.; Chen, S.C.; Soares, H.D.; Morgan, J.I.; Curran, T. Mature 374, 719-723, 1995
A:Title: A protein related to extracellular matrix proteins deleted in the mouse mutant.
A:Reference number: 149297; MUID:95231649; PMID:7715726
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C:Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 11-Jan-2000
C:Accession: S58870; S71844; 149297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 31-Dec-2001
C;Accession: A59386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross_references: EMBL:236531; NID:9535184; PIDN:CAA85298.1; PID:9535185
A;Notes: submitted to the EMBL Data Library, August 1994
Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
210-435/Domain: fibrinogen beta/gamma homology <PGS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                         fibrinogen-like protein expressed in T lymphocytes (pT49) - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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A;Cross-references: EMBL:U24703; NID:g902486; PID:g902487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the Protein Sequence Database, March 2001 A;Reference number: A59386 A;Accession: A59386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 88; DB 2; I 100.0%; Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;Reference number: $71844
A;Accession: $71844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 DRYPSGNCGLYYSSG 378
357 DRYPSGNCGLYYSSG 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DRYPSGNCGLYYSSG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-2403 <SAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-439 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: I37391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; D' Arcangelo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouerv Match
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                                                                                      RESULT 3
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Gaps

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C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999 C;Accession: G71829; G71960 C;Accession: G71829; G71960 G71960 F;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D. ; Ires, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F. Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric p A;Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE001549; GB:AE001439; NID:g4155858; PIDN:AAD06834.1; PID:g415
A;Experimental source: strain J99
A;Accession: G71960
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A;Experimental source: strain Bristol N2; clone F35A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE001459; GB:AE001439; NID:g4154723; PIDN:AAD05786.1; PID:g415
                                                                                                                                                                                                              A;Cross-references: GB:AE002238; GB:AE002161; NID:97189693; PIDN:AAF38579.1; PID:9718
A;Experimental source: strain AR39, HL cells
C;Genetics:
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A; Reference number: A81500; MUID:20150255; PMID:10684935
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C;Accession: 716246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable outer membrane protein - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.3%; Score 42.5; DB 2; Length 696;
                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 2; Length 456;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
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A;Description: The sequence of C. elegans cosmid F35A5.
A;Reference number: 218485
A;Accession: T16246
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0; Mismatches
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Matches 9; Conservative
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Best Local Similarity
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A; Residues: 1-273 <LEI>
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-696 < ARN>
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                                                                                                                                                                                                   -456 <REA>
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                                                                                                                                   A; Accession: A81538
A; Molecule type: DNA
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Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: C86624
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A;Cross-references: GB:AE001687; GB:AE001363; NID:g4377398; PIDN:AAD19207.1; PID:g437740
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R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J. Nature Genet. 21, 385-389, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein CPj1070 [imported] - Chlamydophila pneumoniae (strain J138)
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A; Cross-references: GB:BA000008; NID:g8979443; PIDN:BAA99277.1; GSPDB:GN00142
A; Experimental source: strain J138
                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:272512; PIDN:CAA96667.1; GSPDB:GN00023; CESP:R07B5.7
A;Experimental source: clone R07B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
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C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
                                               C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Accession: T24007
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A;Accession: H72000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Map position: 5
Introns: 31/2; 93/1; 124/3; 194/3; 247/3; 267/3
Superfamily: Caenorhabditis elegans hypothetical protein C33A12.9b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.9%; Score 43; DB 2; Length 339; 53.8%; Pred. No. 26; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                  A;Reference number: 219829
A;Accession: T24007
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                          submitted to the EMBL Data Library, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     est Local Similarity 60.0 atches 6; Conservative
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                       T24007
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Search completed: December 2, 2002, 06:54:03
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A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyperence number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AL139078; GB:AL111168; NID:96968723; PIDN:CAB73857.1; PID:9696886
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Cj1433c [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: Cj1433c
C;Superfamily: Campylobacter jejuni hypothetical protein Cj1433c
                                                                                   Query Match
46.6%; Score 41; DB 2; Length 273;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 8; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 46.6%; Score 41; DB 2; Length 368; Best Local Similarity 70.0%; Pred. No. 58; Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 46.6%; Score 41; DB 2; Length 385; Best Local Similarity 53.3%; Pred. No. 61; Matches 8; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, September 1999 A;Reference number: 220208 A;Accession: 726404
A;Map position: X
A;Introns: 18/3; 62/3; 81/3; 100/3; 140/3; 226/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 58/1; 112/1; 270/2
C;Superfamily: glutamate-ammonia ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: clone Y105C5B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || || || || || || 344 DRRPSSNCDPYTVTG 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DRYPSGNCGLYYSSG 15
                                                                                                                                                                                                             4 PSGNCGLYYSSG 15
                                                                                                                                                                                                                                                                       50 PSGNCGCGSCSG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 PSGNCDNYHS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Residues: 1-368 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-385 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 PSGNCGLYYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CESP: Y105C5B.bb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: A81289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: A81289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: T26404
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hypothetical protein APE2078 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: A/2513
R;Kawarabayasi, Y; HIno, Y; Horikawa, H; Yamazaki, S.; Haikawa, Y.; Jin-no, K; Tawa, H; Takamiya, M; Masuda, S; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
DNA Res. 6, 83-101, 1999
                                                                                                                                                                                                                                                                                               A;Title: Complete genome sequence of an aerobic hyper-thermophijic Crenarchaeon, Aero A;Reference number: A72450; MUID:99310339; PMID:10382966 A;Accession: A72513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: DDBJ:AP000063; NID:95105654; PIDN:BAA81089.1; PID:95105777
A;Experimental source: strain Kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 46.6%; Score 41; DB 2; Length 437; Best Local Similarity 57.1%; Pred. No. 69; Matches 8; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: APE2078
C;Superfamily: conserved hypothetical protein MTH1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RYPSGNCGLYYSSG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A: Molecule type: DNA
A: Residues: 1-437 <KAW>
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: December 2, 2002, 06:41:25 ; Search time 1.25551 Seconds

(without alignments) 495.533 Million cell updates/sec

Title: US-09-902-563-18
Perfect score: 88
Sequence: 1 DRYPSGNCGLYYSSG 15

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 112892 seqs, 41476328 residues

al number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P12804 mus musculu	Q14314 homo sapien	gall	homo sa	mns	rattu	homod		mus r	Q9wuv6 rattus norv	P50603 lymantria d	-					_	human	human a	Q28475 macaca fasc	sacchar	Q12572 candida alb									_	51584 clostridi	Q45715 bacillus th
ΩI	FGL2_MOUSE	FGL2_HUMAN	RELN_CHICK	RELN_HUMAN	RELN_MOUSE	RELN_RAT	CK17_HUMAN	CAZ3_HUMAN	CAZ3_MOUSE	CAZ3_RAT	CHA9_LYMDI	YK78_AERPE	DNB2_ADE07	VP02_BPPRD	UNG_MYCGE	CA21_CHICK	SYPC_METJA	DNB2_ADE41	DNB2_ADE12	AD07_MACFA	ATH1_YEAST	LYS2_CANAL	R27A_ASPOF	R27A_HORVU	R27A_MAIZE	R27A_LYCES	R27A_ARATH	CK17_MOUSE	Y461_SYNY3	SM4B_HUMAN	- 1	XXNY_CLOTM	C1KA_BACTM
n DB	1 7																														4 1	_	ις.
Lengt	432	439	3205	3460	3461	3462	21(299	299	299	12]	437	517	29(245	286	45	474	484	176	121	139.	7	7	7	8	80	21:	42(. 67	75,	107	121
% Query Match Length	100.0	100.0	ς.	ς.	52.3	ď.	Ή.		48.9	48.9							45.5	•		5		44.9	44.3	44.3	44.3	44.3	44.3	44.3	44.3	44.3	44.3	44.3	44.3
Score		88			. 46	46	45	43		43	41	41	41	41	40	40	40	40	40	40	40	39.5	39	39	39	39	39	39	39	39	39	39	39
Result No.	-	2	е	4		9	7	80	6	10		12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q99hv4 brachydanio P78914 schizosacch P20478 drosophila P34497 caenorhabdi P15105 mus musculu P09606 rattus norv P20477 drosophila Q91720 pariacoto v P41320 squalus aca Q9720 parickettsia Q9nyte homo sapien Q01521 podospóra a Q01521 podospóra a	
FSA_BRARE HEM2_SCHPO GIN2_DROME GINA_CAEEL GINA_RAUSE GLNA_RAT GLN1_DROME GLN1_DROME GLN1_DROME GLN1_DROME DNAB_RICPR Z226_HUMAN RPOP_PODDAN	
322 322 365 367 373 373 401 401 486 803	
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4 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	

ALIGNMENTS

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FIBRINGEN C-TERMINAL,
                                                                                                                                                                                                                                                                                                                                                                            /FTId=VAR 013066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Reelin (EC 3.4.21.-) (Fragment).
                                                                                                                                                                                                                 PROSITE: PSOODS1; FIBRIN_AG_C_DOMAIN; 1.
T-cell; Glycoprotein; Signal; Polymorphism.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 3209 AA.
                                                                                                              EMBL; AF104015; AAD10825.1; -.
EMBL; AF604014; AAD10825.1; JOINED.
BEBE; AF468959; AAD168855.1; -.
HSSP; PO2671; 1F2D.
                                                                                                                                                                                  IPR002181; Fibrinogen_C.
                                                                                                                                                                                            Pfam; PF00147; fibrinogen_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                       439 AA; 50228 MW;
                                                                                                  EMBL; 236531; CAA85298.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 DRYPSGNCGLYYSSG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
                                                                                                                                                  02671; 1FZD.
HGNC:3696; FGL2.
                                                                                                                                                                                                                                                         2439
2435
384
253
263
336
53
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DRYPSGNCGLYYSSG 15
                                                                                                                                                                                                          SMART; SM00186; FBG; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    210
213
371
25
179
235
235
263
336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
                                                                                                                                                                         MIM; 605351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RELN_CHICK
                                                                                                                                                                                      InterPro:
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                              Genew;
                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RELN_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yuwaraj S., Liu M., Marsden P., Levy G.; "Cloning and characterization of Hfgl2: the human counterpart to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: MAY PLAY A ROLE IN PHYSIOLOGIC LYMPHOCYTE FUNCTIONS AT
                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marazzi S., Blum S., Hartmann R., Gundersen D., Schreyer M., Argraves S., von Fliedner V., Pytela R., Ruegg C., "Characterization of human fibroleukin, a fibrinogen-like protein
                                                                                             N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Ozuna M., Yi Q., Nickerson D.A.,
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruegg C., Pytela R.; "Sequence of a human transcript expressed in T-lymphocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SUBCELLULAR LOCATION: Secreted.
-: TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC T-CELLS.
                                                                                                                                                                                            Length 432;
                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fibroleukin precursor (Fibrinogen-like protein 2) (pT49).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
                                                                                                                                          N-LINKED (GLCNAC. . .) (PO
A -> G (IN REF. 2).
2B297F69CCB4A782 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                           FIBRINGEN C-TERMINAL.
                                                                                                                                                                                          Score 88; DB 1; I Pred. No. 1.4e-06;
                                                                                                                                                                                                                                                                                                                        PRT; 439 AA.
                                                                      BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUCOSAL SITES.
-!- SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED.
                                                                                                                                                                                                                  0; Mismatches
                                                                                   BY SIMILARITY
                                                  FIBROLEUKIN.
           PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
T-cell; Cytolysis; Signal.
                                   POTENTIAL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND VARIANT GLU-53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding a fibrinogen-like protein.";
Gene 160:257-262(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=7642106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98309432; PubMed=9647217;
                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequ
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                   48951 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secreted by T lymphocytes.";
J. Immunol. 161:138-147(1998).
                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                       100.08;
                                                                                                                                                                                                                15; Conservative
                                                                                                                                                                                                                                                     357 DRYPSGNCGLYYSSG 371
                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                       1 DRYPSGNCGLYYSSG 15
 SMART; SM00186; FBG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Small intestine; MEDLINE-95369700; PubMe
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                 432 AA;
                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                      FGL2_HUMAN
014314:
                                                                      DISULFID
                                                                                                                                                                   SEQUENCE
                                                                                                                               CARBOHYD
                                                                                                                                             CARBOHYD
                                                                                  DISULFID
                                                                                             CARBOHYD
                                                                                                          CARBOHYD
                                                                                                                                                                                          Query Match
                                                                                                                                                       CONFLICT
                                   SIGNAL
                                                         DOMAIN
                                                                                                                                                                                                                                                                                                            FGL2_HUMAN
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                 RESULT 2
Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bernier B., Goffinet A.M.;

Bernier B., Goffinet A.M.;

"Comparative study of realin in vertebrates.";

"Comparative study of realin matrix serine protease that plays a role in layering of neurons in the cerebral cortex and cerebrallum.

"In layering of neurons in the cerebral cortex and receeballum."

Regulates microtubule function in neurons and neuronal migration. Affects migration of sympathetic preganglionic neuronal in the spinal cord, where it seems to act as a barrier to neuronal in the migration. Enzymatic activity is important for the modulation of cell adhesion. Binding to the extracellular domains of lipoprotein receptors viblic and ApoER2 induces Vrosine phosphorylation of Dab1 and modulation of Tau phosphorylation (By similarity).
                                                                                                                                                                                                                                                                                                                        Eukaryoťa; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL).
G -> E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 88; DB 1; Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.5e-06;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DF34656288E49E68 CRC64;
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Matches
                                                                              rmatics and the EMBL outstation.
There are no restrictions on its og as its content is in no way
                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
-i-SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                    Hydrolase; Serine protease; Developmental protein; Matrix protein;
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                                                                              between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81A7B6676BCAA3D1 CRC64;
                                                                                                                                                                                                                                                             Cell adhesion; EGF-like domain; Glycoprotein; Repeat.
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                                -! - SIMILARITY: BELONGS TO THE REELIN FAMILY.
                                         EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                               EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 7.
EGF-LIKE 8.
                                        -!- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAI
-!- SIMILARITY: CONTAINS 15 BNR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46;
Pred. No.
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N-LINKED
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BNR 5.
BNR 6.
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BNR
BNR
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InterPro; IPR000561; EGF-11ke.
InterPro; IPR002860; GH_BNR.
                                                                                                                                                         EMBL; AF090441; AAC35559.1; -.
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                                                                                                                                                                                               Pfam; PF00008; EGF; 4.
Pfam; PF02012; BNR; 15.
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2933
3160
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Best Local Similarity
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CARBOHYD
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71.48;

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MEDLINE-99080080; PubMed-9861036; Impagnatiello F., Guidotti A.R., Pesold C., Dwivedi Y., Caruncho H., Pisu M.G., Uzunov D.P., Smalheiser N.R., Davis J.M., Pandey G.N., Pappas G.D., Tueting P., Sharma R.P., Costa E.; "A decrease of reelin expression as a putative vulnerability factor in schizophrenia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evolutionarily conserved, alternative splicing of reelin during brain
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENAROPCE, Metazoa Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hong S.E., Shugart Y.Y., Huang D.T., Shahwan S.A., Grant P.E., Mucuihane J.O.B., Martin N.D.Y., Walsh C.A.; "Autosomal recessive lissencephaly with cerebellar hypoplasia is associated with human RELN mutations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lamar B., Wamsley P., Gibson A., Maas J., Bauer C., Sapetti L.; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99263436; PubMed=10328932;
Lambert de Rouvroit C., Bernier B., Royaux I., de Bergeyck V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hong S.E., Shugart Y.Y., Huang D.T., Shahwan S.A., Grant P.E., Hourihane J.O.B., Martin N.D.T., Walsh C.A.; Nat. Genet. 27:225-225(2001).
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Indels
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                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                     PRT; 3460 AA.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20428190; PubMed=10973257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exp. Neurol. 156:229-238(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISEASE, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reelin precursor (EC 3.4.21.-).
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10; Conservative
                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                 1722 YPGGNIGLYCPYSS 1735
                                                               3 YPSGNCGLY--YSS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                          P78509; Q9UDQ2;
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL outstation
In Invertion: Extracellular matrix serine protease that plays a role in layering of neurons in the cerebral cortex and cerebellum. Regulates microtubule function in neurons and neuronal migration. Affects migration of sympathetic preganglionic neurons in the spinal cord, where it seems to act as a barrier to neuronal migration. Enzymatic activity is important for the modulation of cell adhesion. Binding to the extracellular domains of lipoprotein receptors VLDLR and ApoRRZ induces tyrosine phosphorylation of Dabl and modulation of Tau phosphorylation (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        schizophrenia. Expression of the protein is reduced (about 50%) in patients with schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- DOMAIN: The basic C-terminal region is essential for secretion (By
                                                                                                                                                                                                                                    **SUBCELLULAR LOCATION: Secreted (By similarity).

-!- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; are produced by alternative splicing.
-!- TISSUE SPECIFICITY: Abundantly produced during brain ontogenesis by the Cajal-Retzius cells and other pioneer neurons located in the telencephalic marginal zone and by granule cells of the external granular layer of the cerebellum. In adult brain, preferentially expressed in GABABATGL interneurons of prefrontal cortices, temporal cortex, hippocampus and glutamatergic granule cells of cerebellum. Also expressed in fetal and adult liver.
-!- DEVELOPMENTAL STAGE: Expressed in fetal and postnatal brain and liver. Expression in postnatal human brain is high in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- DISEASE: Defects in RELN may predispose to autistic disorder. A polymorphic GGC tripler repeat located in the 5'UTR region of RELM (8 to 10 repeats) in the normal population is significantly increased in autistic patients (4 to 23 additional repeats).
-:- SIMILARITY: DELONGS TO THE REELIN FAMILY.
-:- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lissencephaly with cerebelar hypoplasia (Also known as Norman-
Noberts syndrome). Some patients also displayed persistent
lymphedema neonatally, and one showed accumulation of chlyous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1. DISEASE: Defects in RELN are the cause of autosomal recessive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISEASE: Defects in RELN may contribute to susceptibility to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its content
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                                                                                                                                                                                                                             similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cerebellum.
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Gaps
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MISSING (IN ISOFORM 2).
MISSING (IN ISOFORM 3).
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N-LINKED (GLCNAC. . .)
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N-LINKED (GLCNAC. ..)
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N-LINKED (GLCNAC. . .)
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Reelin precursor (EC 3.4.21..) (Reeler protein).
                                                                                                                                                                                                                                                                                                                                                   (GLCNAC.
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N-LINKED (GLCNAC.
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EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 7.
EGF-LIKE 7.
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                                EGF-LIKE 5
EGF-LIKE 6
EGF-LIKE 6
EGF-LIKE 6
EGF-LIKE 6
ENR 1.
ENR 3.
ENR 4.
ENR 4.
ENR 6.
ENR 7.
ENR 7.
ENR 7.
ENR 10.
ENR 11.
ENR 11.
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3460 AA;
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Hydrolase; Serine protease; Developmental protein; Matrix protein;

PROSITE; PS00022; EGF_1; 7. PROSITE; PS01186; EGF_2; 6.

InterPro; IPR000561; EGF-like. InterPro; IPR002860; GH_BNR.

Genew; HGNC:9957; RELN. MIM; 600514; -.

1JV2.

HSSP; P05106;

EMBL;

IPR002861; Reeler.

Pfam; PF00008; EGF; 4.
Pfam; PF02012; BNR; 15.
Pfam; PF02014; Reeler; 1.
SMART; SM00181; EGF; 5.

Cell adhesion; EGF-like domain; Glycoprotein; Repeat; Signal;

Alternative splicing; Lissencephaly

3460

POTENTIAL. REELIN. EGF-LIKE 1.

REELER

DOMAIN SIGNAL

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Radia J., Shinagawa Tunkelliation M., Itoh M., Ishii Y., Arakawa T., Hara A., Shinagawa K., Stawa J., Shinagawa R., Shinagawa R., Shinagawa R., Shinagawa R., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Odkazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radiota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radiota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radiota K., Schmill L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakaii L., Postole G., Quockenbush J., Sakaii L., Mollanda N., Carninci P., de Bonaldo M.F., Blows S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarellii J., Mombaerts P., Lyons P., Marchionni L., Mashima J., Mazzarellii J., Mombaerts P., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storck K.-F., Stozuki H., Toyo-oka K., Wang K.H., Waitz T., Shibata Y., Storck K.-F., Nansaria L., Washawa Boris A., Whittaker C., Whittaker C., Whittaker S., Wansaria V., Nansaria V., Rawaji H., Kohtsuki S., Mansaria V., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                        STRAIN-BALB/C; TISSUE-Brain;
MEDLINE-95375789; PubMed-7647795;
Hirotsune S., Takhara T., Sasaki N., Hirose K., Yoshiki A.,
Ohashi T., Kusakabe M., Murakani Y., Muramatsu M., Watanabe S.,
Nakao K., Katsuki M., Hayashizaki Y.;
"The reeler gene encodes a protein with an EGF-like motif expressed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goffinet A.M.; \mbox{\sc "Evolutionarily conserved, alternative splicing of reelin during brain}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reelin is a secreted glycoprotein recognized by the CR-50 monoclonal
                                      "A protein related to extracellular matrix proteins deleted in the
D'Afcangelo G., Miao G.G., Chen S.-C., Soares H.D., Morgan J.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D'Arcangelo G., Nakajima K., Miyata T., Ogawa M., Mikoshiba K.,
                                                                                                                                                                              Royaux I., Lambert de Rouvroit C., D'Arcangelo G., Demirov D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97325946; PubMed=9182958; Schiffmann S.N., Bernier B., Goffinet A.M.; "Reelin mRNA expression during mouse brain development."; Eur. J. Neurosci. 9:1055-1071(1997).
                                                                                                                                                                                                                        organization of the mouse reelin gene.";
                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=98086481; PubMed=9417911;
                                                                                                                                                                                                                                                                                       SEQUENCE OF 2152-3461 FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 3044-3461 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE-Testis;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21634904; PubMed=11689558;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
MEDLINE=97141547; PubMed=8987733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 277:303-309(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nat. Genet. 10:77-83(1995).
                                                               mouse mutant reeler.";
Nature 374:719-723(1995).
                                                                                                                                                                                                                                                Genomics 46:240-250(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001).
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                                                                                                                                                                                                    Goffinet A.M.;
                                                                                                                                                                                                                          "Genomic
                        Curran T
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produced by alternative splicing.

1. TISSUE SPECIFICITY: The major isoform 1 is neuron-specific. It is abundantly produced during brain ontogenesis by the Cajal-Retzius cells and other ploneer neurons located in the telencephalic marginal zone and by granule cells of the external granular layer of the crebellum. Expression is located in deeper layers in the developing hippocampus and olfactory bulb, low levels of expression are also detected in the immature striatum. At early developing hippocampus and olfactory bulb, low levels of expression are also tected in the immature striatum. At early developmental stages, expressed also in hypothalamic differentiation fields, tectum and spinal cord. A moderate to low level of expression occurs in the septal area, striatal fields, habenular nuclei, some thalamic nuclei, particularly the lateral geniculate, the retina and some nuclei of the reticular formation in the central field of the medulla. Very low levels found in liver and kidney. No expression in radial glial cells, conficial plate, Purkinje cells and inferior clivary neurons. The minor isoform 2 is only expressed in non neuronal cells. The minor isoform 2 is only expressed in non neuronal cells. The minor isoform 2 is only expressed in non neuronal cells. The minor isoform 3 is found in the same cells as isoform 1, but is almost
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Affects migration of sympathetic preganglionic neurons in the spinal cord, where it seems to act as a barrier to neuronal migration. Enzymatic activity is important for the modulation of cell adhesion. Binding to the extracellular domains of lipoprotein receptors VLDLR and ApoBR2 induces tyrosine phosphorylation of Dabl and modulation of Tau phosphorylation.
                                                                                                                                      Hiesberger T., Trommsdorff M., Howell B.W., Goffinet A.M., Mumby M.C.,
                                                                                                                                                                                             "Direct binding of Reelin to VLDL receptor and ApoE receptor 2 induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISEASE: Defects in reln are the cause of the autosomal recessive reeler (rl) phenotype which is characterized by impaired
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DEVELOPENTAL STAGE: First detected at embryonic day 11.5.

EXPRESSION increases up to birth and remains high from post-natal
day 2 to 11 in both cerebellum and fore/midbrain. Expression
                                                                                                                                                                                                                                                                                                                                                                                          Yip J.W., Yip Y.P.L., Nakajima K., Capriotti C.; "Reelin controls position of autonomic neurons in the spinal cord."; Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. FUNCTION: Extracellular matrix serine protease that plays a role in layering of neurons in the cerebral cortex and cerebellum. Regulates microtubule function in neurons and neuronal migration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          motor coordination, tremors and ataxia. Neurons in affected mice fail to reach their correct locations in the developing brain, disrupting the organization of the cerebellar and cerebral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           declines thereafter and is largely brain specific in the adult.
-- DOMAIN: The basic C-terminal region is essential for secretion.
-- PTM: N-glycosylated and to a lesser extent also 0-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBUNIT: Binds to the ectodomains of VLDLR and ApoER2.
-1- SUBCELLULAR LOCATION: Secreted.
-1- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; are
                                                                                                                                                                                                                              tyrosine phosphorylation of disabled-1 and modulates tau
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                                                                                                          MEDLINE-20036019; PubMed-10571241;
                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20359755; PubMed=10880573;
development.";
Exp. Neurol. 156:229-238(1999).
                                                                               BINDING TO VLDLR AND APOER2
                                                                                                                                                                                                                                                                                  Neuron 24:481-489(1999),
                                                                                                                                                                    Herz J.
                                                                                                                                                                                                                                                                                                                                         PUNCTION
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EMBL; U24703; AAB91599.1; -.

us-09-902-563-18.rsp

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"Evolutionarily conserved, alternative splicing of reelin during brain
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                               PROSITE, PS00022; EGF_1; 7.
PROSITE; PS01186; EGF_2; 6.
Hydrolase; Serine protease; Developmental protein; Matrix protein;
                                                                                                                                                                                                                                                                                                                 5;
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Lambert de Rouvroit C., Bernier B., Royaux I., de Bergeyck V.,
                                                                                                      Cell adhesion; EGF-like domain; Glycoprotein; Repeat; Signal;
                                                                                                                                                                                                                                                                                                 Score 46; DB 1; Length 3461;
                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kikkawa S., Terashima T.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 41, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                  PRT; 3462 AA.
                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                               EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 7.
EGF-LIKE 8.
                                                                                                                                          EGF-LIKE 1.
EGF-LIKE 2.
                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                         EGF-LIKE
EMBL; D63520; BAA09788.1; ALT_INIT.
EMBL; AK017094; BAB30592.1; -.
MGD; MGI:103022; Reln.
                                                                                                                                                                                                   BNR
BNR
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                                                                                                                                                                                                                                                                                                                                                                                                                      Reelin precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Created)
                    InterPro; IPR000561; EGF-like.
InterPro; IPR002860; GH_BNR.
                                     InterPro; IPR002861; Reeler.
                                                                SMART; SM00181; EGF; 5.
SMART; SM00001; EGF_like; 2.
                                                                                                                                                                                                                                                                                                  52.3%;
                                          Pfam; PF00008; EGF; 5.
Pfam; PF02012; BNR; 15.
Pfam; PF02014; Reeler; 1.
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                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                               3 YPSGNCGLY--YSS 14
                                                                                                             Alternative splicing.
SIGNAL 1 26
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                                                                                                                                                1001
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                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goffinet A.M.
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                                                                                                                                                                        spinal cord, where it seems to act as a barrier to neuronal migration. Enzymatic activity is important for the modulation of cell adhesion. Binding to the extracellular domains of lipoprotein receptors VLDLR and ApoER2 induces tyrosine phosphorylation of Dabl and modulation of Tau phosphorylation (By similarity). SUBUNIT: Binds to the ectodomains of VLDLR and ApoER2 (By
                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: Secreted (By similarity).
-i- SUBCELLULAR LOCATION: 3 isoforms; 1 (shown here), 2 and 3; are produced by alternative splicing.
-i- TISSUE SPECIFICITY: Abundantly produced during brain ontogenesis by the Cajal-Retzius cells and other pioneer neurons located in the telencephalic marginal zone and by granule cells of the external granular layer of the cerebellum.
-i- DOMAIN: The basic C-terminal region is essential for secretion (By
development.";
Exp. Neurol. 156:229-238(1999).

-:- FUNCTION: Extracellular matrix serine protease that plays a role
-:- FUNCTION: Extracellular matrix serine protease that plays a role
in layering of neurons in the cerebral cortex and cerebellum.
Regulates microtubule function in neurons and neuronal migration.
Affects migration of sympathetic preganglionic neurons in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Serine professe; Developmental protein; Matrix protein;
Cell adhesion; EGF-like domain; Glycoprotein; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SIMILARITŤ: BELONGS TO THE REELIN FAMILY.
-i- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 15 BNR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARG-RICH (BASIC).
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EGF-LIKE 2.
EGF-LIKE 4.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 5.
EGF-LIKE 7.
EGF-LIKE 8.
EGF-LIKE 8.
EGF-LIKE 8.
ENR 1.
ENR 2.
ENR 3.
ENR 5.
ENR 5.
ENR 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB049473; BAB78470.1; -. InterPro; IPR000561; EGF-like. InterPro; IPR002860; GH_BNR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002861; Reeler.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00022; EGF_1; 7. PROSITE; PS01186; EGF_2; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00008; EGF; 5.
Pfam; PF02012; BNR; 15.
Pfam; PF02014; Reeler; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell admes.c., __Alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sampson N., Bikar S.E., Winterpacht A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21418998; PubMed=11528127; Anid C., Bahr A., Milloa A., Sampson N., Bikar S.E., Winterpacht Zabel B., Hankeln T., Schmidt E.R.; "Comparative genomic sequencing reveals a strikingly similar architecture of a conserved systemic region on human chromosome 11p15.3 (including gene ST5) and mouse chromosome 7."; Cytogenet. Cell Genet. 93:284-290(2001).
                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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E 210 AA; 23086 MW; CA3AB6CF4FCD5E59 CRC64;
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MISSING (IN ISOFORM 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                             52.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 71.4 nes 10; Conservative
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3430 343
3430 346
3462 AA;
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-:- SIMILARITY: BELONGS TO THE F-ACTIN CAPPING PROTEIN ALPHA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-2011) to the PMBL/GenBank/DDBJ databases.
-!- FUNCTION: F-ACTIN CAPPING PROTEINS BIND IN A CA(2+)-INDEPENDENT MANNER TO THE FAST GROWING ENDS OF ACTIN FILAMENTS (BARBED END)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H.,
Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
F-actin capping protein alpha-3 subunit (CapZ alpha-3) (GSG3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MORPHOGENESIS OF SPERMATID (BY SIMILARILY).
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.9%; Score 43; DB 1; Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002189; F-actin_cap_A.
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                                                                                                                                                                                                 STANDARD;
95 YTSSQCGKYYSS 106
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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Gaps

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Best Local Similarity 66.78 Matches 8; Conservative

3 YPSGNCGLYYSS 14

131 DHYPKGNCNM 140

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131 DHYPNGNCNV 140

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- TISSUE SPECIFICITY: EXCLUSIVELY EXPRESSED IN THE TESTIS.
-i- DEVELOPMENTAL STAGE: EXPRESSED IN 24-DAY-OLD AND ADULT TESTIS, BUT NOT IN 4-, 10- AND 16-DAY-OLD TESTIS.
-i- SIMILARITY: BELONGS TO THE F-ACTIN CAPPING PROTEIN ALPHA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                    "Isolation and characterization of cDNA clones specifically expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: F-ACTIN CAPPING PROTEINS BIND IN A CA(2+)-INDEPENDENT MANNER TO THE FAST GROWING ENDS OF ACTIN FILAMENTS (BARBED END)
THEREBY BLOCKING THE EXCHANGE OF SUBMITS AT THESE ENDS. UNLIKE
                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
F-actin capping protein alpha-3 subunit (Capz alpha-3) (Germ cell-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yasunaga T., Nishimune Y.; "Genomic analysis of male germ cell-specific actin capping protein
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER CAPPING PROTEINS (SUCH AS GELSOLIN AND SEVERIN), THESE PROTEINS DO NOT SEVER ACTIN FILAMENTS. MAY PLAY A ROLE IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                              Yoshimura Y., Tanaka H., Nozaki M., Yomogida K., Shimamura K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MORPHOGENESIS OF SPERMATID.
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT (BY
                                                                                                                                                                                                                                                                     STRAIN-C57BL/6; TISSUE-Testis;
MEDLINE-95046372; PubMed-7957958;
Tanaka H., Yoshimura Y., Nishina Y., Nozaki M., Nojima H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.9%; Score 43; DB 1; Length 299; 60.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8C87579313F233C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Premis Prolifer.
Probom; PD006960; F-actin_cap_A; 1.
Probom; PD006960; F-actin_cap_A; 1.
PROSITE; PS00748; F-ACTIN_CAPPING_A_1; FALSE_NEG.
PROSITE; PS00749; F-ACTIN_CAPPING_A_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actin-binding; Capping protein; Multigene family, SEQUENCE 299 AA: 34952 MW; 8C87579313F233C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F-actin_cap_A.
                                                      16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB026984; BAA81887.1; -.
MGD; MGI:106221; Cappa3.
InterPro; IPR002189; F-actin_ca
                                                                                                                                                                                                                                                                                                                                                                        in testicular germ cells.";
FEBS Lett. 355:4-10(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D87471; BAA13409.1; -.
                                                                                                                                                CAPZA3 OR CAPPA3 OR GSG3.
                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                              specific protein 3
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY
                    CAZ3_MOUSE
CAZ3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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1 DRYPSGNCGL 10

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                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                         Hurst S., Howes E.A., Coadwell J., Jones R.;
"Expression of a testis-specific putative actin-capping protein
associated with the developing acrosome during rat spermiogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: EXCLUSIVELY EXPRESSED IN THE TESTIS.
SIMILARITY: BELONGS TO THE F-ACTIN CAPPING PROTEIN ALPHA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   MOI. REPIOG. DEV. 49:81-91(1998).
-!- FUNCTION: F-ACTIN CAPPING PROTEINS BIND IN A CA(2+)-INDEPENDENT MANNER TO THE FAST GROWING ENDS OF ACTIN FILAMENTS (BARBED END)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THEREBY BLOCKING THE EXCHANGE OF SUBUNITS AT THESE ENDS. UNLIKE OTHER CAPPING PROTEINS (SUCH AS GELSOLIN AND SEVERIN), THESE PROTEINS DO NOT SEVER ACTIN FILAMENTS. MAY PLAY A ROLE IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eŭkaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HETERODIMER OF AN ALPHA AND A BETA SUBUNIT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
F-actin capping protein alpha-3 subunit (Capz alpha-3),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probon; PD006960; F-actin_cap_A; 1.
PROSITE; PS00748; F-ACTIN_CAPPING_A_2; 1.
PROSITE; PS00749; F-ACTIN_CAPPING_A_2; 1.
Actin-binding; Capping protein; Multigene family.
SEQUENCE 299 AA; 35007 MW; 3D753088BCF79BE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Chorion class A proteins LD9 (Fragment).
Lymantria dispar (Gypsy moth).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPR002189; F-actin_cap_A. Pfam; PF01267; F-actin_cap_A; 1. PRINTS; PR00191; FACTINCAPA.
                                                 PRT;
                                                                                                                                                                                                                                                                                                                   TISSUE=Testis;
MEDLINE=98069272; PubMed=9406198;
                                                                                     6-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MORPHOGENESIS OF SPERMATID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y12538; CAA73137.1; -.
                                               STANDARD;
                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY)
                                          CAZ3_RAT
Q9WUV6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHA9_LYMDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
RESULT 10
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DNB2_ADE07
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                                  InterPro;
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ZN_FING
                                                                                                                                                                                                                                                                                                                    DNB2_ADE07
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                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: MEMBER OF THE ALPHA-BRANCH OF CHORION PROTEIN TO WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawarabayasi Y., Hino Y., Horikwa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sakine M., Baba S.-T., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazahi J., Kushida N., Oguchi A., Aoki K.-T., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                    Lecter R.F., Regier J.C.;
"Evolution of chorion gene families in lepidoptera: characterization of 15 Cohns from the gypsy moth.";
J. Mol. Evol. 39:244-254(1994).
-:- FUNCTION: THIS PROTEIN IS ONE OF MANY FROM THE EGGSHELL OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Insecta, Pterygota; Neoptera, Endopterygota; Lepidoptera; Glossata;
Ditrysia; Noctuoidea; Lymantriidae; Lymantria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.6%; Score 41; DB 1; Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales; Desulfurococcaceae; Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER 1 1 1 S28E28501ED06617 CRC64; SEQUENCE 121 AA; 11617 MW; 528E28501ED06617 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eggshell; Chorion; Repeat; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - SIMILARITY: BELONGS TO THE UBID FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99310339; PubMed=10382966;
                                                                                      TISSUE=Choriogenic follicles;
MEDLINE=95018300; PubMed=7932786;
                                                                                                                                                                                                                                                 BELONG CLASSES A, CA AND HCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein APE2078.
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U04661; AAA67861.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 RYPAGACGI 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=56636;
                                    NCBI_TaxID=13123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aeropyrum pernix.
                                                                                                                                                                                                                GYPSY MOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KK78_AERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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YK78_AERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: BINDS COOPERATIVELY SINGLE-STRANDED DNA IN A SEQUENCE-INDEPENDENT MANNER. INVOLVED IN DNA-REPLICATION, REGULATION OF MRNA FORMATION, AND HOST-RANGE SPECIFICITY. ZINC IS REQUIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: NUCLEAR, ACCUMULATES IN INFECTED CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDILNE-84185604; PubMed=6325415;
Quinn C.O., Kitchingman G.R.;
"Sequence of the DNA-binding protein gene of a human subgroup B
sequence of type 7). Comparisons with subgroup C (type 5) and
subgroup A (type 12).";
J. Biol. Chem. 259:5003-5009(1984).
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                                                                                                                                                                                                   Query Match 46.6%; Score 41; DB 1; Length 437; Best Local Similarity 57.1%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Early protein; DNA-binding; Zinc-finger; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 PHOSPHOKYLATION (1.100-1.)
258 271 POTENTIAL.
517 AA; 58306 MW; A2CC8BIC4AlF191F CRC64;
                                                                                                             Hypothetical protein; Complete proteome.
SEQUENCE 437 AA; 47635 MW; 5055140A80A2D602 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-ANG-1987 (Rel. 05, Created)
13-ANG-1987 (Rel. 05, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
Early E2A DNA-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR005376; Vir_DNA_Zn_bind.
Interpro; IPR003176; Vir_DNA_binding.
Pfam; PP02236; Vir_DNA_binding.
Pfam; PF03728; Vir_DNA_Zn_bind; 2.
                             carboxylyase.
                                                                                  TIGREAMS; TIGR00148; UPF0096; 1.
EMBL; AP000063; BAA81089.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; K02530; AAA42508.1; -.
                                                        Pfam; PF01977; UPF0096; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 NOFSSKSCGMFYTEG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human adenovirus type 7.
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                                                                                                                                                                                                                                                                                                                                                                                             112 REYEGEAGLYLSSG 125
                                                                                                                                                                                                                                                                                                                                     2 RYPSGNCGLYYSSG 15
                          IPR002830;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10519;
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Search completed: December 2, 2002, 06:51:13 Job time: 3.25551 secs
                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                              "Genome organization."
Virology 183:658-676(1991).

Virology 183:658-676(1991).

-1- FUNCTION: THE LIPE CYCLE OF THE PHAGE BEGINS WHEN THE PHAGE ADSORBS TO ITS RECEPTOR ON THE SURFACE OF THE HOST VIA THE ADSORPTION PROTEIN P2 AND INJECTS ITS DNA INTO THE HOST CYTOPLASM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ATCC 33530 / G-37;

BUDLINE-SG02345; bubMed=756993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fleischmann T.D., Weddman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Fleeterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.,
"The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                           MEDLINE-91306449; Pubmed-1853567, Bamford J.K.H., Haenninen A.-L., Pakula T.M., Ojala P.M., Kalkkinen N., Frilander M., Bamford D.H.; "Genome organization of membrane-containing bacteriophage PRDI.";
                                                                                                                       Viruses; dsDNA viruses, no RNA stage; Tectiviridae; Tectivirus.
NCBI_TaxID=10658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.6%; Score 41; DB 1; Length 590; 46.7%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   590 AA; 63690 MW; 5ACA024C92B8F6BC CRC64;
                          01-AUG-1992 (Rel. 23, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNG_MYCGE STANDARD; PRT; 245 AA. P47343, 049318; O1-FEB-1996 (Rel. 33, Created) O1-FEB-1996 (Rel. 33, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Urracil-DNA 91ycosylase (EC 3.2.2.-) (UDG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 1-9.
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; Pubmed-8253680;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 74-231 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 46.79 tes 7; Conservative
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407 DEWVANNCGLFPMSG 421
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                                                                            Adsorption protein P2.
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                                                                                                       Bacteriophage PRD1.
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VP02_BPPRD
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UNG_MYCGE
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72 DPYPSPNDACGLAFAS 87

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels 2; Gaps
                                                                                                                          -:- FUNCTION: EXCISES URACIL RESIDUES FROM THE DNA WHICH CAN ARISE AS A RESULT OF MISINCORPORATION OF DUMP RESIDUES BY DNA POLYMERASE OR DUE TO DEAMINATION OF CYTOSINE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGREAMS; TIGRO0628; ung; 1.
TIGREAMS; TIGRO0628; ung; 1.
PROSITE; PSO0130; 0_DNA_GLYCOSYLASE; 1.
PROSITE; PSO0130; 0_DNA_GLYCOSYLASE; 1.
TO GENERAL BASE (BY SIMILARITY).
TO GENERAL BASE (BY SIMILARITY).
TO SIMILARITY).
TO SIMILARITY.
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE URACIL-DNA GLYCOSYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.5%; Score 40; DB 1; Length 245; 56.2%; Pred. No. 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002043; U_DNA_glycsylse.
InterPro; IPR003249; U_glycosyl.
                                                                                                 Bacteriol. 175:7918-7930(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR005122; UDNA_glycos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U39690; AAC71315.1; -. EMBL; U02201; AAD12490.1; -.
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                                                                        sequencing.
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December 2, 2002, 06:48:20 ; Search time 4.09692 Seconds (without alignments) 754.398 Million cell updates/sec
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                        al number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                               671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                   Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5
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sp_rvirus:*
sp_bacteriap:*
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
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88
1 DRYPSGNCGLYYSSG 15
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sp_phage:*
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Maximum DB seq length: 2000000000
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112:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q9ept7 rattus norv	Q8t8a2 ciona savig	Q9ndq1 ciona intes	Q9y211 homo sapien	Q9y4v9 homo sapien	Q9ugm2 homo sapien	Q9uj57 homo sapien	Q9ukj4 homo sapien	Q96du4 homo sapien	Omor	Q8tae0 homo sapien	Q8tac6 homo sapien	Q9cu50 mus musculu	Q8r0z6 mus musculu	Q9gjh7 salmo trutt	076468 cryptospori
ID	Q9EPT7	Q8T8A2	Q9NDQ1	Q9Y211	Q9Y4V9	Q9UGM2	Q9UJ57	Q9UKJ4	Q96DU4	Q9UGM3	Q8TAE0	QBTAC6	Q9CU50	Q8R026	096лн7	076468
DB	11	Ŋ	ß	4	4	4	4	4	4	4	4	4	11	11	7	S
ğuery Match Length DB	357	220	652	1785	1785	2403	2412	2413	2413	2426	183	210	279	457	217	259
Query Match	100.0	63.6	63.6	52.3	52.3	52.3	52.3	52.3	52.3	52.3	51.1	51.1	9.09	50.6	50.0	50.0
Score	88	26	26	46	46	46	46	46	46	46	45	45	44.5	44.5	44	44
Result No.	1	7	e	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16

PRT; 220 AA.

PRELIMINARY;

Q8T8A2 Q8T8A2; RESULT 2 Q8T8A2 ID Q8T8A AC Q8T8A

Q9vdm9 drosophila Q8tzd1 pyrococcus Q8x33 encephalito Q9qd3 ureaplalito Q9dd13 mus musculu Q2178 caenorhabdi Q3z619 chlamydia p Q8x9rr8 arabidopsis Q8w0r0 sorghum bic Q8r874 thermoanaer Q8z56 halicobacte Q9z390 helicobacte Q9z390 helicobacte Q9z390 helicobacte Q9z390 helicobacte Q9z390 helicobacte Q9z30 leishmania Q8t72e0 leishmania Q8t72e0 leishmania Q8t72e0 leishmania Q8t72e0 leishmania Q8t72e0 helicobacte Q9u377 caenorhabdi Q9tx10 caenorhabdi Q9tx10 caenorhabdi Q9tx10 pamw4 campylobact Q9u377 caenorhabdi Q9w372 porcine age Q9clic9 homo sapien Q8dw8 infectious Q96nm4 homo sapien Q8dw8 infectious Q96nm4 homo sapien	ALIGNMENTS	PRT; 357 AA. 16, Created) 19, Last sequence update) 19, Last sequence update) 19, Last annotation update) 19, Last annotation update) this; Sciurognathi; Muridae; Murinae; Rattus. Phillippe M.; Sprague-Dawley Rat."; the EMBL/GenBank/DDBJ databases. 11, -1; 11, -1. Irinogen_C. I
Q9VDM9 Q8TZD1 Q8SW93 Q9D4N3 Q9D4N3 Q9D4N3 Q8VXR8 Q8WXR8 Q8WXR8 Q8WTE0 Q9NGD0 Q8TTE0 Q9NGD0 Q8TTE0 Q9NGD0 Q8TTE0 Q9DE72 Q9	ALIGN	PRT; 357 16, Created) 16, Last sequence 19, Last annotat data; Craniata; ntia; Sciurognat ntia; Sciurognat the EMBL/GenBank 1; rinogen_C. rinogen_C. rinogen_C rinogen_C rinogen_C
5 111 111 111 111 110 110 110 110 110 11		, 16, 116, 116, 116, 116, 116, 116, 116
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0.008.888888888888884444444444444444444		PRELIMINN 7; R-2001 (TEMBLER R-2001 (TEMBLER R-2001 (TEMBLER IOMBIDIASE FGLZ. S NOVEGGLUS (R 900ta; Metazoa; O 11a; Eutheria; 1 1axID=10116; NOE FROM NA. N-SPRAGUE-DAMLER IX DE., CALGAN REPERSION IN TEM OF CONTROL FROM NA. PPOSTOR (STATE) PPOO147; FIED: NCE 357 AA; tch al Similarity 15; CONSERVE
117 118 119 120 20 20 20 20 20 20 20 20 40 40 40 40 40 40 40 40 40 4		1 199EPT 1-MA-1 1-DB 1-DB 1-DB 1-DB 1-DB 1-DB 1-DB 1-
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PRINTS, PRO0268, SPERACTRCPTR.
SMART; SW00042; CUB; 2.
SMART; SW00202, SR; 9.
SMART; SW00202, SR; 9.
SMART; SW00241; ZP; 1.
                                                                                                                                                                                                                                                                                                                                                               AB020825; BAA78577.1;
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Pfam; PF00530; SRCR; 9.
Pfam; PF00100; zona_pel
                               Homo sapiens (Human).
                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hotta K., Takahashi H., Asakura T., Saitoh B., Takatori N., Satou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                MEDLINE-21920613; PubMed-11923208; Imai K.S., Satoh N., Satou Y.; Satou Y.; Satou Y.; Barly embryonic expression of FGF4/6/9 gene and its role in the induction of mesenchyme and notochord in Ciona savignyi embryos."; EMBL, AB073373; BABB8674.1; -.
                                                                      Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ciona intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                            63.6%; Score 56; DB 5; Length 220; 66.7%; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 63.6%; Score 56; DB 5; Length 652; Best Local Similarity 66.7%; Pred. No. 0.39;
                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB036849; BAB00626.1; -
                                                                                                                                                                                                       NON_TER 1 1 1 SEQUENCE 220 AA; 25758 MW; 4160FAE727F3ED06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro: IPR002181; Fibrinogen_C.
PMan; PF00147; fibrinogen_C; 1.
SMART; SM00186; FG1.
PROSITE: PS00514; FIBRIN.AG_C_DOMAIN; 1.
SEQUENCE 652 AA; 73252 MW; A492Ba325162F0E0 CRC64;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Flbtinogen-1ke protein (Fragment).
CS-FIBRINOGEN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2000 (TrEWBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEWBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                               PRT; 652 AA.
                                                                                                                                                                                                                                                         Pred. No. 0.13
0; Mismatches
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                                                                                  Phlebobranchia; Cionidae; Ciona.
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Conservative
                                                                                                                                                                                                                                                                                                                  143 DGYALGNCGRYYRSG 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intestinalis embryo.";
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P02671; 1FZD,
                                                                                               NCBI_TaxID=51511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                             Ciona savigny
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Q9V211;
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DA LA

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Takeshita H., Sato M., Shiwaku H.O., Semba S., Sakurada A., Hoshi M.,
Hayashi Y., Tagawa Y., Ayabe H., Horii A.,
"Expression of the DMBT1 gene is frequently suppressed in human lung
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PROSITE; PS00120; SRCR_1; UNKNOWN_B.
PROSITE; PS00287; SRCR_2; 9.
PROSITE; PS00682; ZP_DOMATI; UNKNOWN_1.
SEQUENCE 1785 AA; 193991 MW; 38B2363F95226EB0 CRC64;
                                                                                                                                                                                                                                                                         Jpn. J. Cancer Res. 90:903-908(1999).
-!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
EMBL; AB020851; BAA78577.1; --
EMBL; AB020812; BAA78577.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB020813; BAA78577.1; JOINED.
EMBL; AB020814; BAA78577.1; JOINED.
EMBL; AB020815; BAA78577.1; JOINED.
EMBL; AB020816; BAA78577.1; JOINED.
EMBL; AB020817; BAA78577.1; JOINED.
EMBL; AB020818; BAA78577.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000859; CUB_domain.
InterPro; IPR001507; Endoglin/CD105.
InterPro; IPR001190; Srcr_receptor.
                                                                                                              SEQUENCE FROM N.A. MEDLINE=20017478; Pubmed=10551316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAA78577.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB020849; BAA78577.1; JOINED. EMBL; AB020850; BAA78577.1; JOINED.
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AC OC OC OC OC

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A Mollenhauer J., Holmskov U., Wiemann S., Krebs I., Herbertz S., Madsen J., Kloschis P., Coy J.F., Poustka A.;

"The genomic structure of the DMBTI gene: evidence for a region with a susceptibility to genomic instability.";

"The genomic structure of the DMBTI gene: evidence for a region with concepted IB:6213-6240(1999).

"In the genomic structure of the DMBTI gene: evidence for a region with concepted IB:6213-6240(1999).

"In the susceptibility to Genomic in the Proposition of the susception in the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMARI,
SMO241; ZP; 1.
PROSITE; PSO1180; CUB; 2.
PROSITE; PSO0420; SRCR_1; UNKNOWN_13.
PROSITE; PS50287; SRCR_2; 14.
PROSITE; PS00682; ZP_DOMAIN; UNKNOWN_1.
PROSITE; PS00682; ZP_DOMAIN; UNKNOWN_1.
26 2403 DMBTL/8KB.1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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01-MAY-2000 (TrEWBLrel. 13, Last sequence update)
01-UUN-2002 (TrEWBLrel. 21, Last annotation update)
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protein D.;

Proc. Natl. Acad. Sci. U.S.A. 96:10794-10799(1999).

I SIMILARITY: CONTAINS 2 CUB DOMAINS.

EMBL; AJ34212: CAB56155.1;

HSSP; P29392; ISFP.

InterPro; IPR000859; CUB_domain.

InterPro; IPR001507; Endoglin/CD105.

InterPro; IPR001190; Srcr_receptor.
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SMART; SM00202; SR: 14.
SMART; SM00241; ZP; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS00420; SRCR_1; UNKNOWN_13.
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MEDLINE=99415938; PubMed=10485905;
                                                                            MEDLINE=20065089; PubMed=10597221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam PF00431; CUB; 2.
Pfam; PF00530; SRCR; 11.
Pfam; PF00100; zona_pellucida; 1.
PRINTS; PR00258; SPERACTRCPTR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
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           SEQUENCE FROM N.A.
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                                              TISSUE=LUNG;
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           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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   2;
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   1; Indels
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SEQUENCE 1785 AA; 193941 MW; 7B1F8D47E4A82092 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) DMBT1/6kb.1 protein precursor.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNV-2002 (TrEMBLrel. 21, Last annotation update)
DMBT1/8kb.1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q26.1 is deleted in malignant brain tumours.";
                                                                                                                                                                                                                                                                                                                          PRT; 1785 AA.
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   2; Mismatches
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PROSITE; PSO420; SRCR_1; UNKNOWN_8.
PROSITE; PS50287; SRCR_2; 9.
PROSITE; PS00682; ZP_DOMAIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ000342; CONTAINS.
EMBL; AJ000342; CAA04019.1; -
InterPro; IPR001859; CUB_domain.
InterPro; IPR001507; Endoglin/CD105.
InterPro; IPR001190; Srcr_receptor.
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                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
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Pfam: PPO05401; CUB; 2.
Pfam: PPO0100; SRCR: 9.
PFam: PF00100; ZOB_PEIlucida; 1.
SMART; SM0042; CUB; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97434209; PubMed=9288095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nat. Genet. 17:32-39(1997)
9; Conservative
                                                                                                               || ||| ||| |:|:||
1134 PSSNCGGFLFYASG 1147
                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                     4 PSGNCG--LYYSSG 15
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SMART; SM00241; ZP: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=LUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uery Match
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                                                                                                                                                                                                                                                                                                                       09Y4V9
                                                                                                                                                                                                                                                                                                                                                     09Y4V9
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Matches
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SEQUENCE
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SIGNAL
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                                                                                                           2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                            Holmskov U., Mollenhauer J., Madsen J., Vitved L., Gronlund J., Tornoe I., Kliem A., Reid K.B., Poustka A., Skjodt K.; Cloning of gp-340, a putative opsonin receptor for lung surfactant protein D.";
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                  Score 46; DB 4; Length 2412;
Pred. No. 74;
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        SIĞNAL
        1
        25
        POTENTIAL.

        CHAIN
        26
        2412
        DMBTI/8KB.2 PROTEIN.

        SEQUENCE
        2412 AA;
        260568 MW;
        3F630CCBFFB18EDD CRC64;

                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01180; CUB; 2.
PROSITE; PS00420; SRCR_1; UNKNOWN_13.
PROSITE; PS500481; SRCR_2; 14.
SROSITE; PS00682; ZP_DOMAIN; UNKNOWN_1.
SEQUENCE 2413 AA; 260755 MW; 039544043CF463D4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 96:10794-10799 (1999).

-!- SIMILARITY: CONTAINS 2 CUB DOMAINS.

EMBL: AF159456, AAD49696.1;

InterPro: IPR001859; CUB_domain.

InterPro: IPR001180; Endoglin/CD105.

InterPro: IPR001190; Src_receptor.

Pfam: PF00530; SRCR: 14.

Pfam: PF00530; SPERA: 14.

PRINTS: PR00258; SPERACTRCPTR.

SWART: SM00042; CUB; 2.
                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-VUN-2002 (TrEMBLrel. 21, Last annotation update)
DMB11./
                                                                                                                                                                                                                  PRT; 2413 AA.
                                                                                                        2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 74;
2; Mismatches
PROSITE; PS50287; SRCR_2; 14.
PROSITE; PS00682; ZP_DOMAIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=99415938; PubMed=10485905;
                                                                                 52.3%;
64.3%;
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                                                                                                         9; Conservative
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nes 9; Conservative
                                                                                                                                                      1762 PSSNCGGFLFYASG 1775
                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1762 PSSNCGGFLFYASG 1775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00202; SR; 14.
SMART; SM00241; ZP; 1.
                                                                                                                                4 PSGNCG--LYYSSG 15
                                                                                                                                                                                                                                                                         Gp-340 variant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 PSGNCG--LYYSSG 15
                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                  Query Match
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                          Signal.
                                                                                                                                                                                                               Q9UKJ4
Q9UKJ4;
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                                                                                                           Matches
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Q96DU4
                                                                                                                                                                                          RESULT 8
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 DR DR DR DR SO SO
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"Major subforms of DMBTI are gastrointestinal mucins that display extensive alternative splicing and differential protein targeting."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ297935; CAC44122.1; -
InterPro; IRRO00859; CUB_domain.
InterPro; IRRO01507; EnGoglin/CD105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mollenhauer J., Holmskov U., Wiemann S., Krebs I., Herbertz S., Madsen J., Kloschis P., Coy J.F., Poustka A.; "The genomic structure of the DNBT1 gene: evidence for a region with susceptibility to genomic instability.";
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 25 POTENTIAL.
26 2413 DMBTJ/8KB.2 PROTEIN.
2413 AA; 260600 MW; 99A449CSF4F60728 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam: PF00100; zona_pellucida; 1.
PROSITE; PS01180; CUB: 2.
PROSITE; PS00420; SRCR_1; UNKNOWN_13.
PROSITE; PS50287; SRCR_2; 14.
PROSITE; PS00682; ZP_DOMAIN; UNKNOWN_1.
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-!- SIMILARITY: COUPAINS 2 CUB DOMAINS.
EMBL. AJZ43211; CAB63941.1;
InterPro; IPR000859; CUB. domain.
InterPro; IPR001507; Endoglin/CD105.
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PROSITE; PSO0420; SRCR_1; UNKNOWN_13.
PROSITE: PSS0287; SRCR_2: 1.4
PROSITE; PSO0682; ZP_DOMAIN; UNKNOWN_1.
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Pfam; PF00431; CUB; 2.
Pfam; PF00130; SRCR; 14.
Pfam; PF00100; zona_pellucida; 1.
PRINTS; PR00258; SPERACTRCPTR.
SMART; SM0042; CUB; 2.
SMART; SM00242; CUB; 2.
SMART; SM00241; ZP; 14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DMBT1 prototype precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 64.3
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00431; CUB; 2.
Pfam; PF00530; SRCR; 14.
                                                                                                                                                                                TISSUE-SMALL INTESTINE;
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                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                   Mollenhauer J.;
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95 YTSSQCGKYYSS 106
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                    Score 46; DB 4; Length 2426;
Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                            Li R., Han H., Wang J.;
"KBP, a novel protein interacting with LIM protein KoyT.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF493788; AAM12862.1;
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EMBL; AF493786; AAM12865.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.1%; Score 45; DB 4; Length 183; 66.7%; Pred. No. 7.6; ative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 51.1%; Score 45; DB 4; Length 210; Best Local Similarity 66.7%; Pred. No. 8.7; Matches 8; Conservative 0; Mismatches 4; Indels

        SIĞNAL
        1
        25
        POTENTIAL.

        CHAIN
        26
        2426
        DMBTI PROTOTYPE.

        SEQUENCE
        2426 AA;
        262052 MW;
        5A58FBC076FB7247 CRC64;

                                                                                                 1; Indels
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                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
                                                                      52.3%;
                                                                                  64.38;
                                                                                                9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                     Db 1775 PSSNCGGFLFYASG 1788
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                                                                                                                             4 PSGNCG--LYYSSG 15
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                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                      Query Match
Signal.
SIGNAL
CHAIN
                                                                                                                                                                                                                            Q8TAE0
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RECOURTEE FROM N.A.

RECOURTEE FROM N.A. Shinbate M., Shinbate M
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                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similar to angiopoietin-related protein 5.
Mus musculus (Mouse).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.nes.
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279 Aa; 31507 MW; D37B69F61F69C9A5 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PRT; 279 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002181; Fibrinogen_C. Pfam; PF00147; fibrinogen_C; 1. SMART; SM00186; FBG; 1.
                                                                                                                                                                                                                                  6330404E11Rik protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P02671; 1FZD.
MGD; MGI:1917976; 6330404E11Rik.
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 409:685-690(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmo trutta (Brown trout).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDITINE-21147794; Pubmed=11207285;
Shum B.P., Guethlein L., Flodin L.R., Adkison M.A., Hedrick R.P.,
Nehring R.B., Stet R.J.M., Secombes C., Parham P.;
"Modes of Salmonid MHC Class I and II Evolution Differ from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.0%; Score 44; DB 7; Length 217; Best Local Similarity 50.0%; Pred. No. 13; Matches 7; Conservative 3; Mismatches 4; Indels
                              Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025904; AAH25904.1; -.
SEQUENCE 457 AA; 51095 MW; B7C4289E3FEC6C3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC class II beta-chain (Fragment).
                                                                                                                                                                                                                                                                                                                       PRT; 217 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: December 2, 2002, 06:53:26 Job time: 7.09692 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, P01888, IBMG.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003508; Ig_HRC.
InterPro; IPR00353; MHC_II_beta.
Pfam; PP00047; ig; 1.
Pfam; PP00069; MHC_II_beta; 1.
SMART; SM00407; IGcl; I._beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primate Paradigm.";
J. Immunol. 166:3297-3308(2001).
EMBL; AF296399; AAG02545.1; -.
                                                                                                                                                                                                                 391 DSY-SGNCALYHRGG 404
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                                                                                                                                                                                              1 DRYPSGNCGLYYSSG 15
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69 ERYCKGNAAIYYSA 82
SEQUENCE FROM N.A.
TISSUE=LIVER;
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945.247 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908470 seqs, 133250620 residues
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Listing first 45 summaries
                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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88
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1122...
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Human prothrombina	Mouse prothrombina	Human prothrombina	Human angiopoietin	Human gene 1 encod	Novel human diagno	Human SRCR protein	Human SRCR protein	Human reelin prote	Mouse reelin prote
	ID		AAW88236	AAW88235	ABP34223	AAE03347	ABG25291	AAW64590	AAW64591	ABB05007	ABB05008
	ЭВ	20	20	20	23	22	22	19	19	23	23
	Query re Match Length DB 1	15	432	439	53	93	102	999	1785	3460	3461
œ	Query Match	100.0	100.0	100.0	56.8	53.4	52.3	52.3	52.3	52.3	52.3
	Score	88	88	88	20	47	46	46	46	46	46
	Result No.		5	е	4	S	9	7	8	6	10

RRS AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		444495566666666666666666666666666666666	\$52.3 \$52.3 \$51.1 \$51.1 \$51.1 \$51.1 \$51.1 \$51.1 \$51.1 \$51.1 \$51.1 \$6.0 \$48.3 \$48.3 \$48.3 \$48.3 \$48.3 \$47.2 \$46.6 \$46	3461 23 3470 22 3470 22 3470 22 32 22 22 22 22 22 22 22 22 22 22 22	223 222 222 222 222 222 223 223 223 223	ABB57065 ABB57065 AAU800079 AAU800079 AAU800078 AAAU80085 AAU80085 AAM93904 AAM93904 AAM93904 AAM93904 AAM53311 AAM55311 AAM55311 AAM55311 AAM56311 AAM67262 AAY72626 AAY72626 AAY72626 AAY72626 AAY72626 AAY72626 AAM53388 AAM90373	coagulation eranjoublication rany, vaccil	Mouse ischaemic of Novel human diagn Apoptin-association association and Human apoptin-association and Human opptin-association oblypeptid prosophila melano Chlamydia pneumon Chlamydia pneumon Chlamydia pneumon Chlamydia pneumon Chlamydia pneumon Chlamydia pneumon Chlamydia polotic pylori ORF 14 Holicobacter pylori ORF 14 Homan angiopoiet Human naglogenes Human immune/hae Novel human diaglogenes Human immune/hae Sanceriches Novel human diaglogenes Nov
XX SO XX	Ношо	sapiens						
XX	W0985	51335-A1						
XX OF	19-NOV	.v-1998.						
XX PF			0	8WO-CA004	475.			
XX PR PR	10-0CT 15-MAY	T-1997; XY-1997;	97	US-0063	1684. 6537.			
XX PA	(LEVY,	(/) LEVY						
XX PI	Levy	G;						
XX DR	WPI;	1999-05	59687/0	05.				
XIL	Modu]	Modulating i	immune o	coagulation	Latic	tion - by using Fgl2 conditions including	ant	libodies and
7	۲ <u>۱</u>	, 'eninc	วามรูเ	רד עני	3	TETOIIS	grai	יום ברידים היים

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WPI; 1999-059687/05.
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0
                                                                                                                                                                                                        0; Gaps
                                              This peptide corresponds to amino acid residues 364-378 of human prothrombinase Fg12 (see AAW88235). A claimed method of preventing or treating a condition requiring a reduction in immune coagulation comprises administering an inhibitor of Fg12. The inhibitor is preferably an antibody that binds to the Fg12 epitope. The condition to be treated in graft rejection of foetal loss
                                                                                                                                                                                                                                                                                                                                                                                                                Prothrombinase; Fgl2; mouse; immune coagulation; antibody; inhibitor; infection; graft rejection; glomerulonephritis; cancer; gastrointestinal disease; foetal loss; therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used to treat conditions including graft rejection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulating immune coagulation - by using Fg12 antibodies and
                                                                                                                                                                            100.0%; Score 88; DB 20; Length 15; 100.0%; Pred. No. 1e-06;
                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "fibrinogen related domain"
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256..259
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/label= Asn is N-glycosylated
                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                          Mouse prothrombinase Fg12 protein.
                        Claim 4; Page 72; 105pp; English.
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97US-0046537.
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Matches 15; Conservative
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213..439
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                                                                                                                                                     15 AA;
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foetal loss
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                                                                                                                           (claimed).
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                         AAW88236;
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                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Levy G;
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                                                                                                                                                                                                                                                                                         RESULT 2
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allograft and xenograft rejection and foetal loss. An Fgl2-specific antibody, an Fgl2 antisense oligonucleotide, or a substance that affects prothrombinase activity of a Fgl2 protein may be used to treat a condition requiring a reduction in procoagulant activity. A vaccine containing an Fgl2 protein or peptide is used for prevention of graft rejection or foetal loss (claimed).
This is the amino acid sequence of mouse prothrombinase Fg12, as predicted from fg12 DNA (see AAV84140). Fg12 is a 70 kDa transmembrane serine prodease that has immune procoagulant activity. The human Fg12 amino acid sequence is given in AAW88336. The invention provides a method for inhibiting immune coagulation by used in vivo to treat a condition which requires a reduction in immune coagulation such as bacterial and viral infections, cancer, glomerulonephritis, a number of gastrointestinal diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prothrombinase; hfgl2; Fgl2; human; immune coagulation; antibody; inhibitor; infection; graft rejection; glomerulonephritis; cancer; gastrointestinal disease; foetal loss; therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 88; DB 20; Length 432; 100.0%; Pred. No. 2.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Asn is N-glycosylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW88235 standard; Protein; 439 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prothrombinase Fgl2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-CA00475
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Best Local Similarity 100.0
Matches 15; Conservative
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364..37
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predicted from hfg12 DNA (see AAV84139). Fg12 is a 70 kDa transmembrane serine protease that has immune procoagulant activity. The invention provides a method for inhibiting immune coagulation by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           allograft and xenograft rejection and foetal loss. An Fg12-specific antibody, an Fg12 antisense oligonucleotide, or a substance that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                inhibiting the activity or expression of Fg12. The method can be used in vivo to treat a condition which requires a reduction in immune coagulation such as bacterial and viral infections, cancer,
{\tt ModMlating} immune coagulation - by using Fg12 antibodies and compounds, used to treat conditions including graft rejection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treat a condition requiring a reduction in procoagulant activity. A vaccine containing an Fg12 protein or peptide is used for prevention of graft rejection or foetal loss (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           affects prothrombinase activity of a Fg12 protein may be used to
                                                                                                                                                                                                                                  This is the amino acid sequence of human prothrombinase Fg12, as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glomerulonephritis, a number of gastrointestinal diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human angiopoietin-like ORF3196 protein, SEQ ID NO:6392.
                                                                                                                                              Claim 8; Page 66-67; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP34223 standard; Protein; 53 AA.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439 AA;
                                                                               foetal loss
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cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                           hypothyroidism; cholesterol ester storage disease; infection; vulnerary;
Human, ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoliesis regulation; tissue growth, anglogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                    vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antiatherosciertic; antidoagliant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulat dermatological; analgesic; virucide; antibacterial; fungicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAY-2000; 2000US-206690P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
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Sequences AREPJOZA-RAEPSOI TEPTESENT 4334 under procession designated ORP (Open reading frame) 1-4534, and sequences ARN7504-
ABN79587 represent cDNAs encoding them. The invention also encompasses copypeptides at least 80% identical to the ORP-ORF434 (collectively referred to as ORFX) proteins, polynoclecides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX copymoclectides. The recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of screening for modulators of ORFX expression or cartivity, and methods of screening idividuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide cartivity, and methods of screening idividuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide cardivity, and methods of screening idividuals for a predisposition, call differentiation, immune modulation, membolytic activity, chemotractic/ clissue growth, angiogenesis, such as cytokine, cell proliferation, creeptor/ligand, antiinflammatory activity, thrombolytic activity, recoptor/ligand, antiinflammatory activity, tumour inhibition activity, cand antiinfective activity, and may also be involved in the determination and antiinfective activity, and may also be involved in the determination corporated acids and antibodies may be used in the treatment of cancers, corporated acids and antibodies may be used in the treatment of cancers, corporated acids and antibodies may be used in the treatment of cancers, corporated acids and antibodies may be used in the treatment of cancers, corporated acids and antibodies may be used in the treatment of cancers, corporated acids and antibodies may be used in the treatment of cancers, corporated acids and antibodies may be used in the produce of an activity and behaviour. ORFX proteins, corporated acids and antibodies may be used in the produce of an accordance of disorders such as epilepsy and Alzheimer's disease, immune sys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. Offer nucleic acids may also be used as a source of primers and probes, in the detection of Offer genomic sequences or transcripts, in the identification and cloning of homologous sequences, in genetic diagnosis, and in foreneis big of nonlogous which may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX protein, and in drug screening. The ORFX protein may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases.
Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences ABP31028-ABP35561 represent 4534 novel human proteins
                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Page 1846; 2508pp; English.
                                                                                                                                                                                                                                                         transplantation
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0; Gaps 56.8%; Score 50; DB 23; Length 53; 3; Indels Pred. No. 2; 1; Mismatches Local Similarity 66.7 es 8; Conservative 4 PSGNCGLYYSSG 15 20 PSGNCALYHRGG 31 Query Match Matches

53 AA;

Sednence

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foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Human; secreted protein; proliferative disorder; cancer; tumour; Parkinson's disease; cognitive disorder; schizophrenia; asthma; Human gene 1 encoded secreted protein fragment, SEQ ID NO:122. skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; asstrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; AAE03347 standard; peptide; 93 AA. 10-AUG-2001 (first entry) RESULT 5 δy pp

Misc-difference 7

Homo sapiens.

WO200134800-A1.

17-MAY-2001

12-NOV-1999;

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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical immaning of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID No 55650; 103pp; English.
                                                                                                                                                                                  Novel human diagnostic protein #25282.
            ABG25291 standard; Protein; 102 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0649167.
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                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS89478
                                                                                                                                                                                                                                                                                                                                                                              WO200175067-A2
                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                            18-FEB-2002
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                                                                     ABG25291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMD07705-AAD07759 represent cDNAs corresponding to 19 human secreted protein genes, and AAE03292-AAE03346 represent the proteins they encode. CC AAE03347 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene contractions, pathological conditions can be diagnosed by determining the mount of the new protein in a sample or by determining the presence of amount of the new protein in a sample or by determining the presence of amount of the new genes. Specific uses are described for each of the conditions of the second on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of abnormalities, hemanotopiteric disorders, foetal and developmental conditions and the same and products for the diagnosis or treatment of anormalities, hemanotopiteric disorders, foetal and developmental conditions are abnormalities, meurological disorders (e.g., rheumatoid arthritis), inflammation, conditions disposed to soniture disorders, and infections and disorders, and infections and infections are proteins can also be used to aid wound confine and epithelial cell proliferation, to prevent skin aging que to consume the maining and epithelial cell proliferation, to remaining representations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers
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                                                                                                                                                                                                 /note= "X equals stop translation"
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                                                                                                                Location/Qualifiers
                                                                                                                                                                      /label- Unknown
binding partner identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                               08-NOV-2000; 2000WO-US30674.
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30-JUN-2000; 2000US-0215128.
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Best Local Similarity 66.7°
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 PSGNCGLYYSSG 15
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32 PSGNCALYQRGG 43
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Gaps

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Sequence

RESULT 6 ABG25291

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ABB05007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a fragment of a human protein which contains a SRCR (scavenger receptor, oysteine-rich) domain. The gene and encoded protein can be used to diagnose or treat tumours, particularly of the nervous system (medullo-blastoma or glioma) or breast. The DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and probes derived from it, are used to identify genes that express SRCR-domain containing proteins, to determine the form in which these proteins exist and to assess the significance of individual forms on cellular properties. The protein can be used to detect the presence of autoantibodies, and Ab which regulate its expression.
                                                                                   Scavenger receptor cysteine rich domain; SRCR; diagnosis; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scavenger receptor cysteine rich domain; SRCR; diagnosis; treatment; nervous system; medullo-blastoma; glioma; breast; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteins containing scavenger receptor, cysteine rich domain -
                                                                                                   nervous system; medullo-blastoma; glioma; breast; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.3%; Score 46; DB 19; Length 666; 64.3%; Pred. No. 1e+02; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for diagnosis and treatment of tumours
                                                                                                                                                                                                                                                                                                                                                                    (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW64591 standard; Protein; 1785 AA.
                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                       /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1; 54pp; German.
                                                       Human SRCR protein fragment.
                                                                                                                                                                                                                                                                                              98WO-DE00096
                                                                                                                                                                                                                                                                                                                                         97DE-1000519.
                                                                                                                                                                                                                                                                                                                          97DE-1030997
                         23-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  Mollenhauer J, Poustka A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sest Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 PSSNCGGFLFYASG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 PSGNCG--LYYSSG 15
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-399136/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human SRCR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                666 AA;
                                                                                                                                                                                      Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoantibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV49651
                                                                                                               autoantibody.
                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                              09-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                  WO9830687-A2
                                                                                                                                                                                                                                                                                                                          18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                         09-JAN-1997;
                                                                                                                                                                                                                                                                 16-JUL-1998
AAW64590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nery Match
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This sequence represents a human protein which contains a SRCR (scavenger receptor, cysteine-rich) domain. The gene and encoded protein can be used to diagnose or treat tumours, particularly of the nervous system (meduilo-blastoma or glioma) or breast. The DNA sequence and probes derived from it, are used to identify genes that express SRCR-domain containing proteins, to determine the form in which these proteins exist and to assess the significance of individual forms on cellular properties. The protein can be used to detect the presence of autoantibodies and antibodies which regulate its expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; reelin; low density lipoprotein receptor; LDLR; neuroprotective; extracellular glycoprotein; nootropic; antilipeamic; Alzheimer's disease; neurodegenerative disorder: neuronal regeneration; cognitive function; lipid metabolism disease; memory; developmental disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.3%; Score 46; DB 19; Length 1785;
64.3%; Pred. No. 2.7e+02;
itive 2; Mismatches 1; Indels ~ 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteins containing scavenger receptor, cysteine rich domain useful for diagnosis and treatment of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                                                                                                                                                                          (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB05007 standard; Protein; 3460 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human reelin protein SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig 2; 54pp; German.
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                                                                                                                                                                                                                                       97DE-1000519.
                                                                                                                                    98WO-DE00096
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                                                                                                                                                                                                                                                                                                                                                                            Mollenhauer J, Poustka A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 52.37
Best Local Similarity 64.37
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1134 PSSNCGGFLFYASG 1147
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                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-399136/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1785 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV49652
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WO9830687-A2
                                                                                                                                    09-JAN-1998;
                                                                                                                                                                                                      18-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-NOV-2001.
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                                                                                                                                                                                                                                       09-JAN-1997;
                                                                  16-JUL-1998.
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The present invention describes a composition (1) comprising an isolated reelin protein (II) bound to an isolated low density lipoprotein receptor (LDLR) (III). (II) is an extracellular glycoprotein of approximately 385 kba containing a small region of similarity with F-spondin at the N terminus, a stretch of positively charged amino acids at the C terminus, and a series of eight internal repeats of 350-390 amino acids, each repeat containing two related sub-domains that flank a pattern of conserved cysteine residues known as an epidermal growth factor (EGF-like motif. (1) has neuroprotective, noctropic and antilippemic activities, and can be used as a madulator of reelin-LDLR interaction. (I) is, useful in screen for compounds that system comprises a matcroplate array and an automated robotic extracellular glycoprotein; nootropic; antilipaemic; Alzheimer's disease; neurodegenerative disorder; neuronal regeneration; cognitive function; method are useful as therapeutic agents to provide or alleviate a diverse spectrum of diseases including neurodegenerative disorders such Mouse; reelin; low density lipoprotein receptor; LDLR; neuroprotective; as Alzheimer's disease, to facilitate neuronal regeneration after injury, to prevent or alleviate lipid metabolism diseases, to enhance cognitive functions and memory or to ameliorate other developmental disorders. The present sequence represents human reelin, which is used in the exemplification of the present invention. Novel composition useful for screening compounds that modulate Reelin microprocessor controlled system for adding and removing reagents to the microplate array. The compounds identified by the above screening 2; Gaps binding to low density lipoprotein receptor, comprising an isolated Reelin polypeptide and low density lipoprotein receptor 52.3%; Score 46; DB 23; Length 3460; 71.4%; Pred. No. 5.3e+02; tive 0; Mismatches 2; Indels lipid metabolism disease; memory; developmental disorder. (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL. Claim 16; Column 31-48; 45pp; English. ABB05008 standard; Protein; 3461 AA. Mouse reelin protein SEQ ID NO:2. 99US-0334220. 99US-0334220. 21-MAR-2002 (first entry) 10; Conservative Cusran T, D'Arcangelo G; 1973 YPGGNIGLYCPYSS 1986 3 YPSGNCGLY--YSS 14 WPI; 2002-096596/13. Sequence 3460 AA; Best Local Similarity N-PSDB; ABA92603. Mus musculus. US6323177-B1. 16-JUN-1999; 16-JUN-1999; 27-NOV-2001. ABB05008; Query Match Matches RESULT 10 ò

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The present invention describes a composition (1) comprising an isolated realin protein (II) bound to an isolated low density lipoprotein creceptor (LDLR) (III) is an extracellular glycoprotein of receptor (LDLR) (III) is an extracellular glycoprotein of approximately 385 kDa containing a small region of similarity with captoximately 385 kDa containing a small region of similarity with cards are the C terminus, and a series of eight internal repeats of acids at the C terminus, and a series of eight internal repeats of 390-390 anino acids, each repeat containing two related sub-domains contropic and antilipated cysteine residues known as an epidermal growth factor (EGF)-like motif. (I) has neuroprotective, nootropic and antilipatemic activities, and can be used as a modulator of realin-LDLR interaction. (I) is useful in screen for compounds that controllate array and an automated robotic modulate realin binding to an LDLR, in an assay system, where the assay system comprises a microplate array and an automated robotic the microplate array. The compounds identified by the above screening method are useful as therapeutic agents to provide or alleviate a diverse spectrum of diseases including neurodegenerative disorders such a controllate array.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as Alzheimer's disease, to facilitate neuronal regeneration after injury, to prevent or alleviate lipid metabolism diseases, to enhance cognitive functions and memory or to ameliorate other developmental disorders. The present sequence represents mouse (Mus musculus) reelin, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or
                 Novel composition useful for screening compounds that modulate Reelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                        binding to low density lipoprotein receptor, comprising an isolated Reelin polypeptide and low density lipoprotein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse ischaemic condition related protein sequence SEQ ID NO:129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.3%; Score 46; DB 23; Length 3461; 71.4%; Pred. No. 5.3e+02; Live 0; Mismatches 2; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ishii Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ishikawa K, Asai S, Takahashi Y, Nagata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
                                                                                                             Claim 16; Column 47-64; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB57065 standard; Protein; 3461 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 71.4%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 1974 YPGGNIGLYCPYSS 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 YPSGNCGLY -- YSS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-034733/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3461 AA;
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genes (1) In a clear Sample Comprising genes selected from (1). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or wasopsatic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving represent PCR primers for ischaemic claiseases. AB19913 and ABB19914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                           The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.3%; Score 46; DB 23; Length 3461; 71.4%; Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID No 55656; 103pp; English.
                                                     Claim 2; Page 385-400; 2690pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #25288.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 1974 YPGGNIGLYCPYSS 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 YPSGNCGLY--YSS 14
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or treat disease states involving (II). (II) is useful for generating antibodies gainst it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical immaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polymerlectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which encodes an apoptin-associating protein 5 (AAP-5) capable of providing apoptosis, or its functional fragment. The nucleic acid, a vector comprising the nucleic acid, or a proteinaceous substance is susful for the induction of p53-independent apoptosis. The pharmaceutical composition comprising the nucleic acid, vector comprising the nucleic acid or the proteinaceous substance is also useful for the induction of p53-independent apoptosis, or for the treatment of a disease where enhanced cell proliferation or decreased cell death is observed, such as
                                                                                                                                                                                                                                                                                                       diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
     polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated or recombinant nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New apoptin-associating protein 5 for inducing p53-independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 52.3%; Score 46; DB 22; Length 3470; Local Similarity 71.4%; Pred. No. 5.3e+02; nes 10; Conservative 0; Mismatches 2; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cancer; pACT; cytostatic; immunosuppressive; AAP-5; Apoptin-associating protein 5; p53-independent apoptosis; cell proliferation; cell death; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apoptin-associating protein 5 (AAP-5), partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                apoptosis, or for treating cancer or autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Noteborn MHM, Rohn JL, Danen-van Oorschot AAAM;
                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 23; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU80079 standard; Protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-2001; 2001EP-0201137.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1983 YPGGNIGLYCPYSS 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 YPSGNCGLY--YSS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-657960/76.
                                                                                                                                                                                                                                                                                                                                                                                                                              3470 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LEAD-) LEADD BV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enhanced cell proliferation or decreased cell death is observed, such as cancer or autoimmune disease. The present sequence represents the amino acid sequence of apoptin-associating protein 5 (AAP-5).
cancer or autoimmune disease. The present sequence represents the partial amino acid sequence of apoptin-associating protein 5~({\rm AAP}\text{-}5).
                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                      51.1%; Score 45; DB 22; Length 123; 66.7%; Pred. No. 26; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.1%; Score 45; DB 22; Length 126; 66.7%; Pred. No. 27; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apoptin-associating protein 5; p53-independent apoptosis; cell proliferation; cell death; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apoptosis, or for treating cancer or autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer; pACT; cytostatic; immunosuppressive; AAP-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Noteborn MHM, Rohn JL, Danen-van Oorschot AAAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Encoded by pACT vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apoptin-associating protein 5 (AAP-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU80078 standard; Protein; 126 AA.
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                                                                                                                                                                                                    Best Local Similarity 66.73
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                  3 YPSGNCGLYYSS 14
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                                                                                                      Sequence 123 AA;
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                                                                                                                                                                          Query Match
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The invention comprises the amino acid and coding sequences of two apoptin-associating proteins (AAP-5 and AAP-6). The AAP-5/AAP-6 DNA and protein sequences are useful for inducing p53·independent apoptosis, and the diagnosis/treatment (gene therapy) of cancer and autoimmune disease. The AAP-5/AAP-6 DNA and protein sequences are also useful for finding additional apoptin-associating proteinaceous substances from the apoptosis pathway cascade. The present amino acid sequence represents the human AAP-5 protein (with a region derived from the multiple cloning site of the PACT expression vector).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "This region is derived from the multiple cloning site in the pACT expression vector" % \left( \frac{1}{2}\right) =\frac{1}{2}\left( \frac{1}{2}\right) =\frac{1
                                                                                                                                                                                                                                                                                                            Human apoptin-associating protein 5, with pACT expression vector region.
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                                                                                                                                                                                                                                                                                                                                                                                                               Human; pACT expression vector; apoptin-associating protein 5; AAP-5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating cancer and autoimmune diseases comprises the isolated or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "This region represents the human apoptin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.1%; Score 45; DB 23; Length 126; 66.7%; Pred. No. 27; tive 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP-6; p53-independent apoptosis; gene therapy; cancer; autoimmune disease; apoptosis pathway cascade.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Danen-van Oorschot AAAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              associating protein 5 (AAP-5)"
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AA014806 standard; Protein; 126 AA.
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tes 8; Conservative
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                                                                                                       AA014806;
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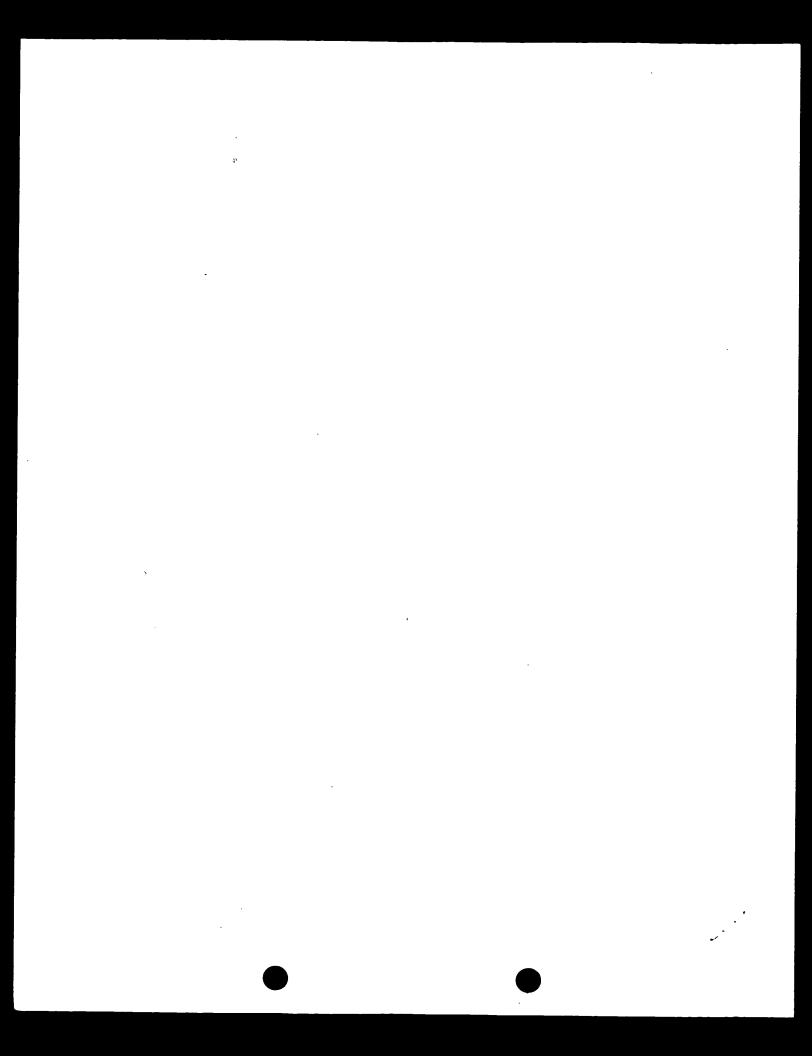
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Gaps

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3 YPSGNCGLYYSS 14

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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: December 2, 2002, 06:53:36; Search time 0.462555 Seconds (without alignments)

516.399 Million cell updates/sec

Title: US-09-902-563-18

Sequence: 1 DRYPSGNCGLYXSG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5
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tal number of hits satisfying chosen parameters: 1023.

102317 seqs, 15924203 residues

Searched:

Animum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

\$ Query

Description	Sequence 2, Appli	Sequence 10, Appl	Sequence 132, App	Sequence 191, App	Sequence 454, App	Sequence 1232, Ap	Sequence 6, Appli	Sequence 14, Appl	quence 39, Appl	Sequence 46, Appl	Sequence 37795, A	Sequence 21, Appl	Sequence 166, App	quence 562, App	Sequence 259, App	Sequence 5153, Ap	Sequence 34, Appl	Sequence 16, Appl	Sequence 16, Appl
Desc	Sec	Se	Se	Se	Se	Se	Sed	Sed	Se	Se	Se	Sed	Se.	Se	Se	Se	Sed	Sed	Sed
ID	0 US-09-819-308-2	0 US-09-819-308-10	2 US-10-001-870-132	0 US-09-764-898-191	2 US-10-052-586-454	0 US-09-925-300-1232	US-09-344-882-6	US-09-344-882-14	0 US-09-785-632A-39		10 US-09-864-761-37795	US-10-125-452-21	12 US-10-006-867-166	2 US-10-052-586-562		0 US-09-815-242-5153	US-10-125-452-34	US-10-125-470-16	US-10-125-452-16
Query Match Length DB ID	126 1	10 1	16 1	695 1	837 1	69	31 9	406 9	•		-	•				181 1	77 9	778 9	78 9
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Query Match	51.1	51.1	45.5	44.3	44.3	43.8	43.8	43.8	43.2	43.2	42.6	42.0	42.0	42.0	42.0	42.0	42.0	42.0	42.0
Score	45	45	40	39	39	38.5	38.5	38.5	38	38	37.5	37	37	37	37	37	37	37	37
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Sequence 4, Appli Sequence 9, Appli Sequence 4, Appli Sequence 2, Appli Sequence 7, Appli Sequence 7, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 17, Appli Sequence 17, Appli Sequence 10, Appli Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 35273, A Sequence 3, Appli Sequence 35273, A Sequence 3589, A Sequence 34, Appli
9 US-10-020-733-4 9 US-10-125-470-9 10 US-09-933-511A-4 9 US-10-020-733-8 9 US-10-020-733-8 9 US-10-020-733-8 12 US-10-020-734-9 12 US-10-027-348-9 12 US-10-027-348-9 12 US-10-027-348-9 12 US-10-027-348-14 12 US-10-027-348-14 10 US-09-280-197-5 10 US-09-280-197-5 10 US-09-907-185-10 10 US-09-907-187-10 10 US-09-907-187-10 10 US-09-861-289-10 10 US-09-861-761-3498-10 10 US-09-864-761-3498-10
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APPLICANT: No. US20020019040Aleborn, Mathleu
APPLICANT: Danen-van Oorschot, Astrid
APPLICANT: Rohn, Jennifer
ITILE OF INVENTION: APOPTIN-ASSOCIATING PROTEIN
FILE REFERENCE: 2906-4830US
CURRENT APPLICATION UNDER: US/09/819,308
UGRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 46
                                                                             GENERAL INFORMATION:
APPLICANT: No. US202019040Aleborn, Mathieu
APPLICANT: Danen van Oorschot, Astrid
APPLICANT: Banen van Oorschot, Astrid
APPLICANT: Rohn, Jennifer
TITLE OF INVENTION: APOPPIN ASSOCIATING PROTEIN
FILE REFERENCE: 2906-4820US
CURRENT APPLICATION NUMBER: US/09/819,308
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; Patent No. US20020019040A1
                           Sequence 2, Application US/09819308; Patent No. US20020019040A1
                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: vector pMT2SM-AAP-5
US-09-819-308-2
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US-09-819-308-2
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/052266
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR PELLOCATION NUMBER: 60/063120
PRIOR PILING DATE: 1997-10-24
PRIOR PELLING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR PILING DATE: 1997-10-21
PRIOR PELLING DATE: 1997-10-21
PRIOR PELLING DATE: 1997-10-21
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R APPLICATION NUMBER: 60/066466
R FILING DATE: 1997-11-24
R APPLICATION NUMBER: 60/066772
R FILING DATE: 1997-11-24
R APPLICATION NUMBER: 60/069335
                                                                                                                                                                                                             ; Sequence 454, Application US/10052586
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PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-29
PRIOR PELING DATE: 1997-10-29
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
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APPLICATION NUMBER: 60/077649
FILING DATE: 1998-03-11
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FILING DATE: 1997-11-13
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APPLICATION NUMBER: 60/069425
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APPLICATION NUMBER: 60/069870
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Wood, William I.
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Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                              Desnoyers, Luc
Goddard, Audrey
                                                                                                                                                                                                                                                                                                        APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                      ; Patent No. US20020127584A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: P3430R1C1
                                             321 YPGGMCLPYYST 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pan, James
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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APPLICANT:
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APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
FILE REFERENCE: DEX-0283
                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                               Ouery Match 51.1%; Score 45; DB 10; Length 210; Best Local Similarity 66.7%; Pred. No. 5.7;
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                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/001,870
                                                                                                                                 ; ORGANISM: open reading frame of AAP-5 US-09-819-308-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 132, Application US/10001870 Patent No. US20020150924A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,189
PRIOR FILING DATE: 2000-11-21
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; Patent No. US20020090673A1
; SOFTWARE: Patentin version 3.0; SEQ ID NO 10
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
                                                                                                                                                                                                                                                                                              8; Conservative
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US-09-764-898-191
                                                                                                                                                                                                                                                                                                                                                         3 YPSGNCGLYYSS 14
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US-10-001-870-132
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                                                                                                     TYPE: PRT
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PRIOR APPLICATION NUMBER: 00/081838
PRIOR FILING DATE: 1998-04-15
PRIOR PLING DATE: 1998-04-15
PRIOR FILING DATE: 1998-04-21
PRIOR FILING DATE: 1998-04-21
PRIOR PRICATION NUMBER: 60/082569
PRIOR PRICATION NUMBER: 60/082704
PRIOR PRIOR DATE: 1998-04-22
PRIOR PRIOR DATE: 1998-04-22
PRIOR PLING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08453
PRIOR PLING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087208
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/081049
PRIOR PELLING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILLING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR PELLORATION NUMBER: 60/081195
                                                                                                                                                                              PRIOR FILLING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILLING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080107
                                                                        PRIOR APPLICATION NUMBER: 60/078939
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PRIOR APPLICATION NUMBER: 60/080194
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PRIOR APPLICATION NUMBER: 60/080333
PRIOR #PPLICATION NUMBER: 60/078886
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                                                                                                         1998-03-20
                                    PRIOR FILING DATE: 1998-03-20
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Gaps
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5; Indels
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PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089908
                                                                               APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088028
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APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
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FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/089512
APPLICATION NUMBER: 60/087759
                                                                                                                                               FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
                                                                                                                                                                                         FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/088212
FILING DATE: 1998-06-05
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-09
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APPLICATION NUMBER: 60/088811
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                FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827
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Matches 7; Conservative
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APPLICANT: Ke, Jinshan
APPLICANT: Johnson, Jerry L
APPLICANT: Allred, Carcolyn C
APPLICANT: Fatland, Beth
APPLICANT: Lutziger, Isabelle
APPLICANT: Wen, Tsui-Jung
TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and
TITLE OF INVENTION: Accetyl CoA Levels in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 43.2%; Score 38; DB 10; Length 23; Best Local Similarity 54.5%; Pred. No. 7.6; Matches 6; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kim, Jin-Soo
APPLICANT: Kim, Jin-Soo
APPLICANT: Kwon, Young Do
APPLICANT: Kim, Hyun-Won
APPLICANT: Ryu, Eun-Hyun
APPLICANT: Ryu, Eun-Hyun
APPLICANT: Ryu, Eun-Hyun
APPLICANT: Ryu, Eun-Hyun
APPLICANT: INFORMATION: ZINC FINGER DOMAINS AND METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 12279-002001
CURRENT APPLICATION NUMBER: US/09/785,632A
CURRENT FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 166
SOFTWARE: FASTEED for Windows Version 4.0
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 201573
CURRENT APPLICATION NUMBER: US/09/344,882
CURRENT FILING DATE: 1999-06-25
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                                                                                                          Behal, Robert
Schnable, Patrick S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis Thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1998-06-26
                          Nikolau, Basil J
Wurtele, Eve S
Oliver, David J
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1998-06-2
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PAtentIn Ver. 2.2
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       GENERAL INFORMATION:
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                                                                                                       APPLICANT:
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                                  APPLICANT:
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APPLICANT: Oliver, David J

APPLICANT: Behal, Robert

APPLICANT: Schnable, Patrick S

APPLICANT: Ke, Jinshan

APPLICANT: Aliver or oliver, Johnson, Jerry L

APPLICANT: Lutziger, Isabelle

APPLICANT: Lutziger, Isabelle

APPLICANT: Wen, Tsui-Jung

TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and

TITLE OF INVENTION: Acetyl CoA Levels in Plants

FILE REFERENCE: 201573

CURRENT APPLICATION NUMBER: US/09/344,882

CURRENT FILING DATE: 1999-06-25

FRIOR APPLICANTION NUMBER: US 60/090,717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 43.8%; Score 38.5; DB 10; Length 69; Best Local Similarity 42.1%; Pred. No. 18; Matches 8; Conservative 2; Mismatches 2; Indels 7
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                                                                     APPLICANT: Stewe Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
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                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/925,300 CURRENT FILING DATE: 2001-08-10
                                                                                                                                                    PRIOR APPLICATION UNMBER: PCT/USO0/05988
PRIOR FILING DATE: 2000-03-08
PRIOR PLICATION NUMBER: PCT/USO0/05988
                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
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; Patent No. US20020162137A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Arabidopsis Thaliana
US-09-344-882-6
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                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
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; Patent No. US20020151681A1
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                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                               APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
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                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1232
LENGTH: 69
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Matches

RESULT 8

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4; Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 0.64
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.71
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
OTHER INFORMATION: SWISSPROT HIT: P34618, EVALUE 2.40e-01
OTHER INFORMATION: EST_HUMAN HIT: BE390050.1, EVALUE.1.00e-81
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                                                             PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 37795
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PRIOR APPLICATION NUMBER: 09/712,907
PRIOR FILLING DATE: 2000-11-16
PRIOR FILLING DATE: 2000-01-16
PRIOR PELICATION NUMBER: PCT/US00/14308
PRIOR PELICATION NUMBER: 60/178,717
PRIOR PELICATION NUMBER: 60/178,717
PRIOR PELICATION NUMBER: 60/142,930
PRIOR FILING DATE: 1999-07-09
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CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 09/955,504
                   PRIOR APPLICATION NUMBER: US 60/234,687
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; Patent No. US20020173640A1
                                                    PRIOR FILING DATE: 2000-09-21
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
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                                                                                                           AFFLICATION AUTHORNIAN MINISTRANCE COMPOUND MODULATION OF Fas Mediated Signaling FILE REFERENCE: ISPH-545
CURRENT APPLICATION NUMBER: US/09/802,669
CURRENT FILING DATE: 2001-03-09
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
RIOR APPLICATION NUMBER: US 09/290,640
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 180
SOFTWARE: PALENTIN VET. 2.0
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PRIOR PAPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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Patent No. US20020048763A1
GENERAL INFORMATION:
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APPLICKNT: Dean, Nicholas M.
APPLICANT: Macusson, Eric G.
APPLICANT: Wyatt, Jacqueline
APPLICANT: Zhang, Hong
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
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APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS BNCOOLNG THE SAME
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PRIOR APPLICATION NUMBER: 60/08297
PRIOR PILING DATE: 1998-04-22
PRIOR PELING DATE: 1998-04-29
PRIOR PELING DATE: 1998-04-29
PRIOR PELING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-07
PRIOR PILING DATE: 1998-06-07
PRIOR PELING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-04
PRIOR PELING DATE: 1998-06-04
PRIOR PELING DATE: 1998-06-07
PRIOR PELING DATE: 1998-06-07
PRIOR PELING DATE: 1998-06-10
PRIOR PELING DATE: 1998-06-12
Sequence 166, Application US/10006867 Patent No. US20020119130A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/064215
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091628
PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-08-18
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Grimaldi, Christopher J.
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APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
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R APPLICATION NUMBER: 60/101475
R FILING DATE: 1998-09-23
R APPLICATION NUMBER: 60/101738
R FILING DATE: 1998-09-24
R APPLICATION NUMBER: 60/101743
R FILING DATE: 1998-09-24 APPLICATION NUMBER: 60/102570 FILING DATE: 1998-09-30 APPLICATION NUMBER: 60/096959 FILING DATE: 1998-08-18 APPLICATION NUMBER: 60/097954 APPLICATION NUMBER: 60/097971 FILING DATE: 1998-08-26 APPLICATION NUMBER: 60/099812 FILING DATE: 1998-09-10 APPLICATION NUMBER: 60/099815 FILING DATE: 1998-09-10 FILING DATE: 1998-09-16 APPLICATION NUMBER: 60/100683 FILING DATE: 1998-09-17 APPLICATION NUMBER: 60/101279 FILING DATE: 1998-09-22 APPLICATION NUMBER: 60/103449 FILING DATE: 1998-10-06 APPLICATION NUMBER: 60/103678 FILING DATE: 1998-10-08 PRIOR APPLICATION NUMBER: 60/103679
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103711
PRIOR FILING DATE: 1998-10-08 APPLICATION NUMBER: 60/108807 FILING DATE: 1998-11-17 APPLICATION NUMBER: 60/112419 FILING DATE: 1998-12-15 APPLICATION NUMBER: 60/097979 APPLICATION NUMBER: 60/099741 FILING DATE: 1998-09-10 APPLICATION NUMBER: 60/099763 FILING DATE: 1998-09-10 APPLICATION NUMBER: 60/099792 APPLICATION NUMBER: 60/100684 FILING DATE: 1998-09-17 APPLICATION NUMBER: 60/100930 APPLICATION NUMBER: 60/101916 APPLICATION NUMBER: 60/105000 FILING DATE: 1998-10-20 APPLICATION NUMBER: 60/106030 FILING DATE: 1998-10-28 APPLICATION NUMBER: 60/106856 FILING DATE: 1998-11-03 APPLICATION NUMBER: 60/112853 FILING DATE: 1998-12-16 APPLICATION NUMBER: 60/113011 FILING DATE: 1998-12-16 APPLICATION NUMBER: 60/098749 APPLICATION NUMBER: 60/100627 FILING DATE: 1998-09-16 APPLICATION NUMBER: 60/100662 APPLICATION NUMBER: 60/105002 PRIOR APPLICATION NUMBER: 60/112422 APPLICATION NUMBER: 60/106464 APPLICATION NUMBER: 60/105881 FILING DATE: 1998-08-26 FILING DATE: 1998-08-26 FILING DATE: 1998-09-10 FILING DATE: 1998-10-20 1998-10-30 FILING DATE: 1998-09-01 FILING DATE: 1998-09-17 FILING DATE: 1998-12-15 FILING DATE: 1998-10-2

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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PRIOR APPLICATION NUMBER: 60/059263
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APPLICATION NUMBER: 60/063540
FILING DATE: 1997-10-28
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FILING DATE: 1997-12-18
APPLICATION NUMBER: 60/077450
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PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
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PRIOR APPLICATION NUMBER: 60/059266
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PRIOR FILING DATE: 1997-10-24
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FILING DATE: 1997-10-28
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PRIOR FILING DATE: 1997-10-28
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APPLICATION NUMBER: 60/063870
FILING DATE: 1997-10-31
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FILING DATE: 1997-10-31
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PRIOR FILING DATE: 1998-03-11
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PRIOR FILING DATE: 1998-03-20
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FILING DATE: 1998-03-31
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APPLICATION NUMBER: 60/080327
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                                                                                                                      Watanabe, Colin K.
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           Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                Wood, William I.
                                                                                         Smith, Victoria
                                                                                                                                                                                                                                                       FILE REFERENCE: P3430R1C1
                                                                                                                                                                          Zhang, Zemin
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PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
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Goddard, Audrey
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PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
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PRIOR PELICATION NUMBER: 60/082569
PRIOR PELICATION NUMBER: 60/082569
PRIOR PELICATION NUMBER: 60/082704
PRIOR PELICATION NUMBER: 60/082704
PRIOR PELICATION NUMBER: 60/08379
PRIOR PELICATION NUMBER: 60/083495
PRIOR PELICATION NUMBER: 60/084639
PRIOR PELICATION NUMBER: 60/084639
PRIOR PELICATION NUMBER: 60/084639
PRIOR PELICATION NUMBER: 60/084640
PRIOR PELICATION NUMBER: 60/085573
PRIOR APPLICATION NUMBER: 60/085573
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PRIOR FILING DATE: 1938-05-28
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
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PRIOR PELLING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILLING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088025
PRIOR APPLICATION NUMBER: 60/088025
PRIOR PELLING DATE: 1998-06-04
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080333
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PRIOR APPLICATION NUMBER: 60/087098
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PRIOR FILING DATE: 1998-06-04
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                                                                           FILING DATE: 1998-04-01
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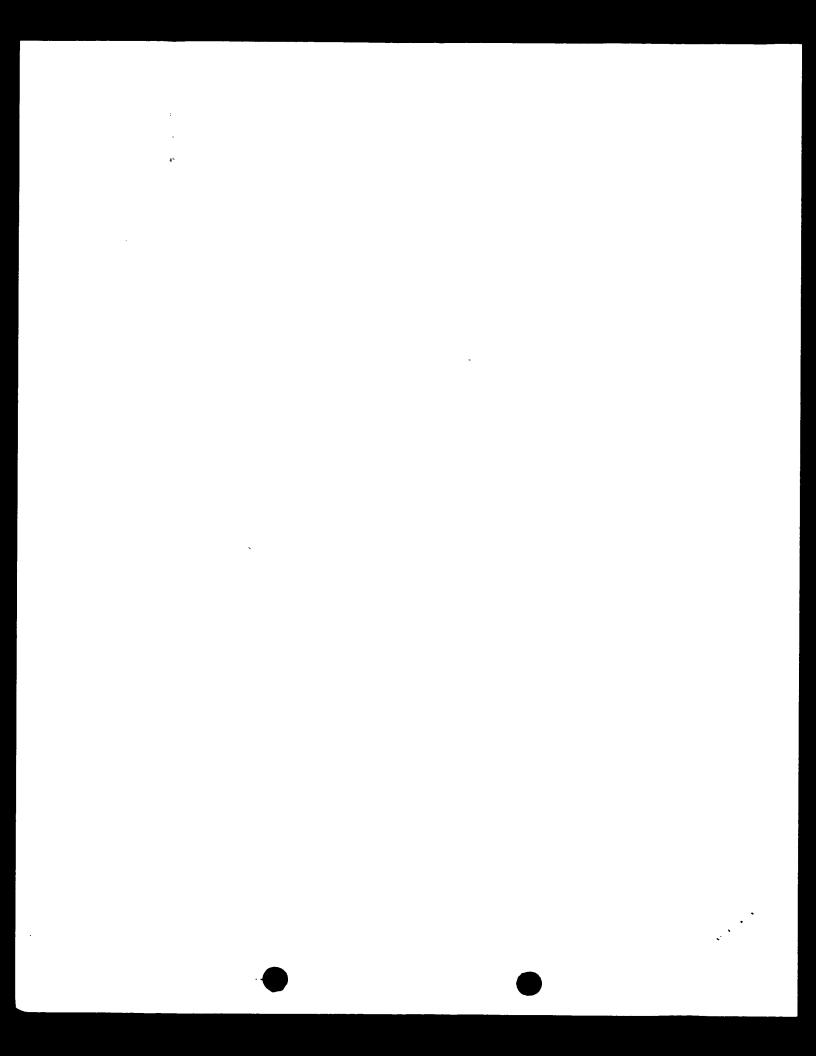
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TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
FILE REFERENCE: 078003-0271150
CURRENT APPLICATION NUMBER: US/09/886,055
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PRIOR FILING DATE: 1998-06-09
PRIOR PLING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/213,812
PRIOR FILING DATE: 2000-06-22
                    FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-12
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PRIOR FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/088217
FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088655
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PRIOR APPLICATION NUMBER: 60/089538
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
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APPLICANT: STRYER, 1
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SOFTWARE: Patentin Ver. 2.1

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; SEQ ID'MO 259
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-055-259
Query Match
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 GNCGLYY 12
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Search completed: December 2, 2002, 07:00:07 Job time : 1.46256 secs



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Sequence 4, Appli
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                                                                   December 2, 2002, 06:49:20 ; Search time 0.89207 Seconds (without alignments) 494.741 Million cell updates/sec
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Sequence 19,
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Sequence 1,
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                         262574 seqs, 29422922 residues
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                                              OM protein - protein search, using sw model
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28	38.5	43.8	406	4	US-09-108-020-42	Sequence 42, Appl
29	38	43.2	2465	7	US-08-596-291-3	3, 8
30	38	43.2	2465	m	US-09-100-804-3	
31	38	43.2	2466	e	US-09-080-855-12	12
32	38	43.2	2466	Ŋ	PCT-US94-09943-2	
33	38	43.2	2485	4	US-09-290-640-46	
34	37	42.0	393	٣	US-09-127-124-1	
35	37	42.0	393	4	US-08-979-170-2	
36	36.5	41.5	70	4	US-09-165-827C-9	6
37	36.5	41.5	284	4	US-09-165-827C-14	
38	36.5	41.5	342	4	US-09-165-827C-2	7
39	36.5	41.5	549	æ	US-08-886-886-13	=
40	36.5	41.5	551	ĸ	US-08-886-886-15	15,
41	36.5	41.5	1066	~	US-08-633-770A-1	1, 7
42	36	40.9	116	m	US-09-184-658-48	48
43	36	40.9	233	7	US-07-890-422B-1	
44	36	40.9	265	4	US-09-199-637A-57	57
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; Patent	Patent No. 6403089	03089)		-
; GENERA	GENERAL INFORMATION: APPLICANT: LAVY GA	MATION: evv. Gar	>			
; APPLI	CANT: (APPLICANT: Clark, David A.	Javid A			
; TITLE	OF INV	ENTION:	Method	0	TITLE OF INVENTION: Methods of Modulating Immune Coagulation	ulation
; FILE	REFEREN	FILE REFERENCE: 9579-14	9-14			

Query Match 100.0%; Score 88; DB 4; Length 15; Best Local Similarity 100.0%; Pred. No. 3.2e-07; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps

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US-09-442-143A-4

Sequence 4, Application US/09442143A
Fatent No. 6403089
GENERAL INFORMATION:
APPLICANT: Levy, Gary
APPLICANT: Clark, David A.
TITLE OF INVENTION: Methods of Modulating Immune Coagulation
FILE REFERENCE: 9579-14
CURRENT APPLICATION NUMBER: US 60/0442,143A
CURRENT FILING DATE: 1999-11-15
FRIOR FILING DATE: 1997-05-17
FRIOR FILING DATE: 1997-05-17
FRIOR FILING DATE: 1997-05-17
FRIOR APPLICATION NUMBER: US 60/061,684
FRIOR FILING DATE: 1997-10-10
FRIOR FILING DATE: 1997-10-10
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1

SEQ ID NO 4

LENGTH: 432

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1785
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                                                                                                                                                                                                                                                                              SEO ID NO 3
                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                           RESULT 5
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                                                                             Length 432;
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APPLICANT: Clark, David A.
TITLE OF INVENDENCY: Methods of Modulating Immune Coagulation
FILE REFERENCE: 9579-14
CURRENT APPLICATION NUMBER: US/09/442,143A
CURRENT FILING DATE: 1999-11-15
PRIOR APPLICATION NUMBER: US 60/046,537
PRIOR FILING DATE: 1997-05-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 439;
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TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REFERENCE: 4121-108
                                                                       100.0%; Score 88; DB 4; I
100.0%; Pred. No. 9.4e-06;
tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 15; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/061,684
PRIOR FILING DATE: 1997-10-10
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/09442143A ; Patent No. 6403089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09341587 Patent No. 6346606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1
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Matches 9; Conservative
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                                                                                        Best Local Similarity 100.
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                                                                                                                                                                               357 DRYPSGNCGLYYSSG 371
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; TYPE: PRT
; ORGANISM: Murine fgl2
US-09-442-143A-4
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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US-09-442-143A-2
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APPLICANT: St. Judes Children's Research Hospital
APPLICANT: Curran, Thomas
APPLICANT: Unrangelo, Gabriella
APPLICANT: D'Arcangelo, Gabriella
TITLE OF INVENTION: INTERACTION OF REELIN WITH VERY LOW
TITLE OF INVENTION: THERAPIES
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TITLE OF INVENTION: INVERACTION OF REELIN WITH VERY LOW
TITLE OF INVENTION: DENSITY LIPOPROTEIN (VLDL) RECEPTOR FOR SCREENING AND
TITLE OF INVENTION: THERAPIES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                     TITLE OF INVENTION: Protein Containing an SRCR Domain FILE REFERENCE: 4121-108 CURRENT APPLICATION NUMBER: US/09/341,587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
BARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
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CURRENT APPL/CEATION NUMBER: US/09/334,220
CURRENT FILING DATE: 1999-06-16
NUMBER OF SEC ID NOS: 5
US-09-341-587-3
; Sequence 3, Application US/09341587
; Patent No. 6346606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-334-220-1
; Sequence 1, Application US/09334220
; Patent No. 6323177
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Matches 9; Conservative
                                                                                 GENERAL INFORMATION:
APPLICANT: Mollenhauer, Jan
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Matches 10; Conservative
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APPLICANT: St. Jude
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                                                                                                                                                                                                                                52.3%; Score 46; DB 4; Length 3461; 71.4%; Pred. No. 1.5e+02; tive 0; Mismatches 2; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                         FastSEQ for Windows Version 3.0
                            CURRENT APPLICATION NUMBER: US/09/334,220
CURRENT FILING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 5
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APPLICATION NUMBER: US/08/933,821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GOdowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
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Sequence 6, Application US/08933821
Patent No. 5972338
GENERAL INFORMATION:
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; Patent No. 6057435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             South San Francisco
California
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Amino Acid
FILE REFERENCE: 2427/0F704
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                                                                                                                                                                                                                                                                          10; Conservative
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                                                                                                                                                                        ; ORGANISM: Mus musculus US-09-334-220-2
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Best Local Similarity
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Matches 9; Conserva
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                                                                                                                                LENGTH: 3461
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                                                                                                             SEO ID NO 2
                                                                                                                                                      TYPE: PRT
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5; Indels 1; Gaps
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                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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CURRENT APPLICATION DATA:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
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; Patent No. 6350450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
                                                                                                              ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 470 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 60.0 Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DRYPSGNCGLYYSSG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                              536
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                                                                                                                                                                                                                             94080
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
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                                                                                                                                                                                                        COUNTRY:
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; Patent No. 6413770
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                                                                                                                                                                                                5; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels 1; Gaps
                                                                                                                                                           47.2%; Score 41.5; DB 4; Length 470; 60.0%; Pred. No. 94; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.2%; Score 41.5; DB 4; Length 470; 60.0%; Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,928A
FILING DATE: 14-Jun-1999
CLASSIFICATION: <0nknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
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SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/933,821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: «Unknown»
ATTORBEY AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Godowski, Paul J.
Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                           S-09-332-928A-6
Sequence 6, Application US/09332928A
Patent No. 6368853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 470 anino acids
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               TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 17
                                                                      1: 470 amino acids
Amino Acid
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Best Local Similarity 60.00,
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650/225-3216
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                                                                                     TYPE: Amino Acia
TOPOLOGY: Linear
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TELEPHONE:
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                                                                      LENGTH:
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                                                                                                                                                               Query Match
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5; Indels 1; Gaps
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                               APPLICANT: Tumas, Daniel
APPLICANT: Schwall, Ralph
TITLE OF INVENTION: Tie Ligand Homologues
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/136,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P1130P2
                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
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Patent No. 6420542
                                                                                                              APPLICANT: Roy, Margaret APPLICANT: Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055
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TELECOMMUNICATION INFORMATION:
                  Godowski, Paul J.
                                  Gurney, Austin
Hillan, Kenneth
Botstein, David
Goddard, Audrey
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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1 DNA Way
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                                                                                                                                                                                                                                                                                    CITY: South San Francisco
STATE: California
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California
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Matches 9; Conservative
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                           USA
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STREET: 1 [
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                  APPLICANT:
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ORGANISM: Calisoga sp.
                      INDIVIDUAL ISOLATÉ: ;
ORGANELLE: Venom gl.
US-08-390-882A-1
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APPLICANT: Kral, Robert M. Jr.; Krapcho, Karen; Johnson,
TITLE OF INVENTION: Insecticidal Peptides from Spider Venom
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                   47.2%; Score 41.5; DB 4; Length 470; 60.0%; Pred. No. 94; rive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette, 3.50 inch, 1.44 Mb storage
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ADDRESSEE: AMSSON & METCALF
STREET: 950 FIRST INTERSTATE BUILDING
STREET: 170 SOUTH MAIN STREET
CITY: SALT LAKE CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WORDFERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,882A
FILING DATE: No. 5588764e assigned
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: L. CRAIG METCALF
REGISTRATION NUMBER: 31,398
REFERENCE/DOCKET NUMBER: 1094.2.1
TELECOMUNICATION INFORMATION:
TELEPHONE: (801) 537-1700
                    APPLICATION NUMBER: US/09/332,929
                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: P1130 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08390882A Patent No. 5688764
                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/933,821
                                                                                                                                                     NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                             TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS-DOS
                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         LENGTH: 470 amino acids TYPE: Amino Acid
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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ORIGINAL SOURCE:
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                                                                                                                FILING DATE:
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                                         FILING DATE
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TELEFAX: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-390-882A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                -09-332-929-6
                                                                                                                                                                                                                                                                                                                                                                                                       uery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kral, Robert M. Jr.; Krapcho, Karen; Johnson, Ja
TITLE OF INVENTION: Insecticidal Peptides from Spider Venom
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 46.6%; Score 41; DB 1; Length 39; Best Local Similarity 40.0%; Pred. No. 9.1; Matches 8; Conservative 3; Mismatches 1; Indels
                                                                                                   46.6%; Score 41; DB 1; Length 39; 40.0%; Pred. No. 9.1;
                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette, 3.50 inch, 1.44 Mb storage
                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MADSON & METCALF
STREET: 950 FIRST INTERSTATE BUILDING
STREET: 170 SOUTH MAIN STREET
CITY: SALT LAKE CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: December 2, 2002, 06:54:36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/390,882A FILING DATE: No. 5688764e assigned CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/08390882A
; Patent No. 5688764
ISULATE: peptide A Venom glands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOLATE: peptide B
Venom glands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: L. CRAIG METCALF
REGISTRATION NUMBER: 31,398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 537-1700
                                                                                                                                                                                                 2 RYP-----SGNCGLYYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RYP----SGNCGLYYS 13
                                                                                                                                                                                                                                                5 RYPCSNSKDCCSGNCGTFWT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 RYPCSNSKDCCSGNCGTFWT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (801) 537-1799
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                           Query Match
Best Local Similarity 40.vv.
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Calisoga sp. INDIVIDUAL ISOLATE: pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

December 2, 2002, 07:00:11 ; Search time 55 Seconds (without alignments) 26.218 Million cell updates/sec

US-09-902-563-18

88 1 DRYPSGNCGLYYSSG 15 Perfect score: Sequence:

283224 seqs, 96134422 residues Searched:

Gapop 10.0 , Gapext 0.5

BLOSUM62

Scoring table:

ptal number of hits satisfying chosen parameters:

Maximum DB seq length: 15 nimum DB seq length: 0

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

PIR_73:* Database :

pir1:* pir2:* pir3:* pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result	gross	Query	1000th	2	4	
	1000	110000	TICHOCK!	9 :	TO	Describeron
П	31	35.2	14	7	A58963	alpha-conotoxin Cn
7	31	35.2	15	Н	NTKNAG	
3	56	29.5	15	7	PQ0017	
4	24	27.3	10	7	C41946	T-cell receptor da
2	23.5	26.7	12	7	825056	Id heavy chain - m
9	23	26.1	10	7	PT0243	
7		26.1	13		JTJG3	merode
ω	23	26.1	14	7	PH0792	T-cell receptor al
Q	23	26.1	15	7	PH1366	Iq heavy chain DJ
10	23	26.1	15	~	PH0750	T-cell receptor be
11	23	26.1	15	~	PL0110	complement factor
12	22.5	25.6	11	7	B41946	T-cell receptor ga
13	22	25.0	6	~	S19329	activating
14	22	25.0	11	ď	PT0302	Iq heavy chain CRD
15	22	25.0	13	Н	NTKN2G	alpha-conotoxin GI
16	22	25.0	13	ď	150173	alpha-2 collagen -
17	22	25.0	14	Н	NTKNIM	alpha-conotoxin MI
18	22		14	~	PH1305	Id heavy chain DJ
19	22		15	~	C37765	hypothetical prote
20	21	٠	6	~	PT0288	
21	21	23.9	6	7	G41946	T-cell receptor ga
22	21		σ	7	PD0027	pev-tachykinin - p
23	21	٠	10	~	B38887	T-cell receptor qa
24	21	٠	11	7	PH1584	
25	21	٣,	12	7	H41946	T-cell receptor da
26	21	23.9	13	~	A28953	alpha-conotoxin ŠI
27	21	<u>.</u>	13	7	A61210	antibiotic GE2270
28	21	23.9	15	7	PT0085	protein QA600027 -
53	21	23.9	15	7	S47387	T-cell antigen rec

acidic fibroblast	epidermal growth f	T-cell receptor be	acetylcholinestera	Iq H chain V-D-J r	botulinum neurotox	botulinum neurotox	Iq heavy chain CRD	Iq H chain V-D-J r	aspartate transami	hypertrehalosemic/	proteasome chain 1	T-cell receptor al	T-cell receptor al	porin por 1B - Ara	porin porl - Arabi
803955	S08301	PT0652	568637	PH1596	S58862	S58866	PT0252	PH1597	A11483	A31571	209082	PH0802	PH0788	PA0109	PA0045
7	7	7	7	7	7	7	7	7	N	7	~	7	7	7	7
15	15	9	11	13	14	14	14	14	7	10	12	13	13	14	14
23.9	23.9	22.7	22.7	22.7	22.7	22.7	22.7	22.7	21.6	21.6	21.6	21.6	21.6	21.6	21.6
21	21	20	20	20	20	20	20	20	19	19	19	19	19	19	19
30	. 31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

A58963 alpha-conotoxin CnIA - cone shell (Conus consors) (Contains: alpha-conotoxin CnIB	RESULT 1			
(Conus	158963			
V:Contains: alpha-conotoxin CnIB	1pha-conotoxin CnIA - cone	shell	(Conus	consors)
	V;Contains: alpha-conotoxin	CnIB		

C;Species: Conus consors C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999 C; Accession: A58963

R;Favreau, P.; Krimm, I.; Le Gall, F.; Bobenrieth, M.J.; Lamthanh, H.; Bouet, F.; Ser Biochemistry 38, 6317-6326, 1999
A;Title: Biochemical characterization and nuclear magnetic resonance structure of nov A;Reference number: A58963; MUID:99255390; PMID:10320362

A; Status: preliminary A; Accession: A58963

A. Molecule type: protein
A. Mesidues: 1.14 < FRAV>
C; Superfamily: alpha-conotoxin
C; Superfamily: alpha-conotoxin
C; Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu
C; Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu
C; Keywords: acetylcholine receptor inhibitor; amidated canboxyl end (CIB #status experimental <MATB>
F; 3-14/Product: alpha-conotoxin CIIB #status experimental
F; 3-44/A/Disulfide bonds: #status experimental
F; 14/Modified site: amidated carboxyl end (Cys) #status experimental

0; Gaps Query Match 35.2%; Score 31; DB 2; Length 14; Best Local Similarity 83.3%; Pred. No. 1.1e+02; Matches 5; Conservative 0; Mismatches 1; Indels

; 0

8 CGLYYS 13 8 CGKYYS 13 QQ δλ

RESULT 2

alpha-conotoxin GIA [validated] - cone shell (Conus geographus)

N'Alternate names: alpha-CTx-GIA N'Contains: alpha-conotoxin GI

C;Species: Conus geographus (geography cone) C;Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 15-Sep-2000

Rigray, W.R.; Luque, A.; Olivera, B.M.; Barrett, J.; Cruz, L.J. J. Biol. Chem. 256, 4734-4740, 1981
A;Title: Peptide toxins from Couns geographus venom.
A;Reference number: A92320; MUID:81191854; PMID:7014556 C; Accession: A01782

A; Accession: A01782

A; Molecule type: protein
A; Residues: 1-15 cGRA>
A; Residues: 1-15 cGRA>
B; Galy, M.R.; Rivier, J.E.; Galyean, R.; Cruz, L.J.; Olivera, B.M.
J. Biol. Chem. 256, 12247-12251, 1983
A; Title: Conotoxin MI. Disulfide bonding and conformational states.
A; Reference number: A92396; MUID: 84032400; PMID: 6630187
A; Contents: annotation; disulfide bonds
R; Guddat, L.W.; Shan, L.; Martin, J.L.; Edmundson, A.B.; Gray, W.R.

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A; Description: In situ studies on the primary immune response to (4-hydroxy-3-nitroph A; Reference number: $25024 A; Accession: $25056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R'Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. D. Exp. Med. 173, 395-407, 1991. Astribe: Preferential utilization of specific immunoglobulin heavy chain diversity an A; Reference number: PT0222; MUID:91108337; PMID:1899102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Sakagami, Y.; Yoshida, M.; Isogai, A.; Suzuki, A.
Science 212, 1525-1527, 1981
A;Title: Peptide sex hormones inducing conjugation tube formation in compatible matin
A;Reference number: A94256
                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Mus musculus (house mouse)
C.Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
C.Accession: S255056
R.Jacob, J.; Kelsoe, G.
submitted to the EMBL Data Library, July 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain CRD3 region (clone 2-103A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tremerogen a-13 - jelly fungus (Tremella mesenterica)
C;Species: Tremella mesenterica
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 07-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Cross_references: EMBL:X67386; NID:950927; PIDN:CAA47798.1; PID:91333920 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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ص
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.7%; Score 23.5; DB 2; Length 12;
46.2%; Pred. No. 1.5e+03;
tive 0; Mismatches 2; Indels
                                                                               Score 24; DB 2; Length 10;
Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.1%; Score 23; DB 2; Length 10; 71.4%; Pred. No. 1.5e+03; tive 0; Mismatches 2; Indels
                                                                                                                                            2; Indels
                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1.10 cYAM>
A;Experimental source: B lymphocyte
C;Keywords: heteroretramer; immunoglobulin
                                                                               27.3%; 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.28;
                                                                                                          Local Similarity 50.0 nes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 46.29
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-12 <JAC>
             C; Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RYPSGNCGLYYSS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RYP----YYYGS 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                      Iq heavy chain - mouse
                                                                                                                                                                                                              8 CGLYYSSG 15
                                                                                                                                                                                                                                                                        2 CAVWSSSG 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: PT0243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: PT0243
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                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Submitted to the Brookhaven Protein Data Bank, May 1996
A; Reference number: A66253; PDB:1NOT
A; Contents: annotation; X-ray crystallography, 1.2 angstroms, residues 1-13
A; Guddat, L.W.; Martin, J.A.; Shan L.; Edmundson, A.B.; Gray, W.R.
Biochemistry 35, 11329-11335, 1996
A; Title: Three-dimensional structure of the alpha-conotoxin GI at 1.2 angstroms resoluti
A; Reference number: A58592; MUID:96378624; PMID:8784187
A; Contents: annotation; X-ray crystallography, 1.2 angstroms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F.1-15/Product: conotoxin GIA #status experimental <GIA>
F.1-13/Product: conotoxin GI #status experimental <GIC>
F.1-13/Product: conotoxin GI #status experimental <GIC>
F.2-7,3-13/Disulfide bonds: #link GIA #status predicted
F.2-7,3-13/Disulfide bonds: #link GIC #status experimental
F.13/Modified site: amidated carboxyl end (Cys) (amide in mature form from following gly)
F.15/Modified site: blocked carboxyl end (Lys) (probably amidated) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: C41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Reference number: A41946
A;Reference number: A41946
                                                                                                                                                                                                                                                              Ribardi, A.; Galdes, A.; Florance, J.; Manicontc, D. Babchemistery 28, 5494-5501, 1989 Blochemistery 28, 5494-5501, 1989 Blochemistery 28, 5494-5501, 1989 A:Title: Solution structures of alpha-concoxin GI determined by two-dimensional NMR spe A:Reference number: A30629; MUID:89375269; PMID:2775719 A:Contents: annotation; conformation by (1)H-NMR C;Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynapt C;Superfamily: alpha-conotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 84, 247-255, 1989
A;7tle: Primary structure of bacteriophage M2 DNA polymerase: conserved segments within A;Reference number: JQ0161; MUID:90128268; PMID:2515115
A;Accession: PQ0017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; blocked carboxyl en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Sep-1999
C:Accession: PQ0017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;MOJecule type: DNA
A;Residues: 1-15 <MAT>
A;Cross-references: GB:M33144; NID:g215507; PIDN:AAA32367.1; PID:g215508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; not compared with conceptual translation A;Wolecule type: DNA A;Residues: 1-10 <WHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31; _____Pred. No. 1.2e+02; _____hnes 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.5%; Score 26; DB 2; Length 15; 50.0%; Pred. No. 7.3e+02; Live 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.2%; Score 31; DB 1; Length 15; 62.5%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-cell receptor gamma chain (1t.60) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Matsumoto, K.; Takano, H.; Kim, C.I.; Hirokawa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Superfamily: phage PZA terminal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      terminal protein - phage M2 (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 62.54
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DRYPSGNCGL 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 CGLYYSSG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 CGRHYSCG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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C; Species: Mus musculus (house mouse)
C; Date: 03-Reb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C; Date: 03-Reb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C; Accession: B41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma A;Reference number: A41946; MUID:92049316; PMID:1658619
                                                                                                                             A,Title: T cell receptor genes in a series of class I major histocompatibility comple allelic exclusion and antigen-specific repertoire.

A;Reference number: PHO746; MUID:92078846; PMID:1836010

A;Accession: PHO750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement factor B1-Bb and B2-Bb - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Species: 13.Mar-1990 #sequence_revision 31-Mar-1990 #text_change 15-Nov-1996
C;Accession: PL0110
R;Matsushita, M.; Okada, H.
Mol. Immunol. 26, 669-676, 1989
A;Title: Two forms of guinea pig factor B of the alternative complement pathway with A;Reference number: A93136; MUID:89384686; PMID:2779589
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                  C;Accession: PH0750
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.6%; Score 22.5; DB 2; Length 11; 55.6%; Pred. No. 2e+03; ative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 26.1%; Score 23; DB 2; Length 15; Best Local Similarity 37.5%; Pred. No. 2.2e+03; Matches 3; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 2; Length 15;
Pred. No. 2.2e+03;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 1-15 <MAT>
C;Keywords: complement alternate pathway; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-cell receptor gamma chain (1t.57) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: T lymphocyte C; Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 26.1%;
Best Local Similarity 44.4%;
                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: X06841
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Matches 5; Conservative
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A, Residues: 1-11 <WHE>
C, Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 CGLY-YSSG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CAVWRYSSG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 PSGNCGLYY 12
                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-15 <CAS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 PSGNCGLY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 PAGSMNIY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: PL0110
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A; Title: Predominance of fetal type DJH joining in young children with B precursor lymph A; Reference number: PH1302; MUID:93094761; PMID:1460419
A; Accession: PH1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Title: T cell receptor genes in a series of class I major histocompatibility complex-rallelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
                                                                                                                                                                C.Keywords: extracellular protein; hormone; lipoprotein; pheromone; prenylated cysteine F:13/Binding site: farnesyl (Cys) (covalent) #status experimental F:13/Modified site: methyl ester carboxyl end (Cys) #status absent
                                                                     |Residues: 1-13 <SAK>
| Comment: Tremerogen a-13 is_produced by the a mating-type cells and induces formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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ate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell receptor alpha chain (H2 V-alpha-2.TA19) - mouse (Iragment)
Species: Mus musculus (house mouse)
Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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J. Exp. Med. 174, 1371-1383, 1991
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                                                                                                                                                                                                                                                                                             26.1%; Score 23; DB 1; Length 13; 80.0%; Pred. No. 1.9e+03; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.1%; Score 23; DB 2; Length 14; 45.5%; Pred. No. 2.1e+03; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain DJ region (clone C111-106) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T-cell receptor beta chain (C11) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-15 <WAS>
C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X60897
A;Experimental source: T lymphocyte
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Matches 5; Conservative
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                                                                                                                                       C;Superfamily: tremerogen a-13
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                      A; Molecule type: protein
A; Residues: 1-13 <SAK>
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A: Residues: 1-15 <WAS>
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          A; Accession: A01641
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                                                                                                                                                                                                                                                                                                                                                                                                                                 4 PSGNC 8
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Search completed: December 2, 2002, 07:03:59 Job time: 56 secs
                                                                                                                 8 CGLYYS 13
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7 CGKHFS 12
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                                                                                                                                                                                               A;Title: Determination of the amino acid sequence of an intramolecular disulfide linkage
A;Reference number: S19329; MUID:92097763; PMID:1756858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rigray, W.R.; Rivier, J.E.; Galyean, R.; Cruz, L.J.; Olivera, B.M.
J. Biol. Chem. 258, 12247-12251, 1983
A; Title: Conotoxin MI. Disulfide bonding and conformational states.
A; Reference number: A92396; MUID:84032400; PMID:6630187
A; Contents: annotation; disulfide bonds
C; Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynapt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Superfamily: alpha-conotoxin
C.Keywords: acetylcholine receptor inhibitor; blocked carboxyl end; postsynaptic neurotc
F:2-7,3-13/Disulfide bonds: #status predicted
F:13/Modified site: blocked carboxyl end (Cys) (probably amidated) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
L. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A:Reference number: Pr0222; MUID:91108337; PMID:18999102
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sperm-activating peptide SAP - sea urchin (Stomopneustes variolus)
C;Species: Stomopneustes variolus
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Aug-2000
C;Accession: S19329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Homo sapiens (man)
C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
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C.Date: 24-Sep-1981 *sequence_revision 24-Sep-1981 *text_change 23-May-1997
C.Rocession: A01783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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J. Biol. Chem. 256, 4734-4740, 1981
A;Title: Peptide toxins from Conus geographus venom.
A;Reference number: A92320; MUID:81191854; PMID:7014556
A;Accession: A01783
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.0%; Score 22; DB 2; Length 9; Best Local Similarity 60.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.0%; Score 22; DB 2; Length 11; 1larity 71.4%; Pred. No. 2.4e+03; Conservative 0; Mismatches 2; Indels
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                                                                                                                               R;Yoshino, K.; Takao, T.; Shimonishi, Y.; Suzuki, N. FEBS Lett. 294, 179-182, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha-conotoxin GII - cone shell (Conus geographus)
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                                                                                                                                                                                                                                                                                        A.Molecule type: protein
A.Residues: 1-9 <VOS>
C.Superfamily: unassigned animal peptides
F;3-8/Disulfide bonds: #status predicted
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nes 5; Conserva
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A; Residues: 1-13 <GRA>
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A; Residues: 1-11 <YAM>
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3 GPRYSSG 9
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Gaps
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            25.0%; Score 22; DB 1; Length 13; 50.0%; Pred. No. 2.8e+03; tive 2; Mismatches 1; Indels
Query Match
Best Local Similarity 50.0.,
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

December 2, 2002, 06:54:40; Search time 11 Seconds (without alignments) 56.559 Million cell updates/sec Run on:

US-09-902-563-18 88 1 DRYPSGNCGLYYSSG 15 Title: Perfect score:

Sequence:

Scoring table: BLOSUM62 Gapext 0.5

112892 segs, 41476328 residues Searched:

748 tal number of hits satisfying chosen parameters:

Maximum DB seq length: 0 Maximum DB seq length: 15

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dР			SUMMARIES	
Result No.	Score		ŭ	DB	ID	Description
1	31	35.2	14	-	CXA1 CONCN	P56973 conus conso
7	31		15	П	CXA1_CONGE	couns
m	26	29.5	15	1	TERM_BPM2	bacter
4	23	26.1	13	Н	TA13_TREME	
2	23	26.1		П	MARI_ALTSP	P29399 alteromonas
9	23	26.1	15	П	UC14_MAIZE	
7	22	25.0		-	SAP_STOVA	
	22		-	7	CXA2_CONGE	
0	22			Н	CXA1_CONMA	couns
10	21			П	TRP4_LEUMA	leucop
11	21		-	П	C1QA_RAT	P31720 rattus norv
12	21	23.9	7	П	FGF1_CANFA	_
13	20		10	-	PPCK_FASHE	
14	19			-	TKL1_LOCMI	
15	19	21.6		1	HTF_HELZE	<u>-</u>
16	19			Н	SCK3_LEIQU	
17	19			Н	TA1_TREBR	P34070 tremella br
18	19			Π	UC06_MAIZE	
19	18				AMPN_HELAM	P81731 helicoverpa
20	18				UHA1_HUMAN	
21	18		14	Н	CAT2_FASHE	P80342 fasciola he
22	18		14	-	HY14_PIG	P01155 sus scrofa
23	18		14	Н	LPER_BACLI	_
24	18		15		KLOM_LUMTE	P11918 lumbricus t
25	18		15	Н	UC19_MAIZE	
26	17		8	,	ALL1_CYDPO	
27	17		œ		LCK8_LEUMA	
28	17		σ	-	- 1	_
29	17		6	-		P32878 oryctolagus
30	17		12	-		5
31	17	19.3	14	Η.	SODN_STRGR	32
32	17		15	-	OBPA_MAMBR	P81285 mamestra br
33	16		∞	-	ALL6_CYDPO	io

P83047 conus ventr P80982 thunns obe	P11735 locusta mig P11496 periplaneta P81350 clostridium	P41869 calliphora P82021 litoria inf			
COW_CONVE	CU30_LOCMI CORZ_PERAM UN05_CLOPA	FARI_CALVO FRE1_LITIN	LICH_BACLI RF1_CONSP	LPAA_PORGI MP1_MICOC	ALYT_ALYOB
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ALIGNMENTS

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"Solution conformation of conotoxin GI determined by 1H nuclear magnetic resonance spectroscopy and distance geometry calculations."; Biochemistry 28:4853-4860(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Groebe D.R., Dumm J.M., Levitan E.S., Abramson S.N.; "alpha-Conotoxins selectively inhibit one of the two acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hann R.M., Pagan O.R., Eterovic V.A.;
"The alpha-conotoxins GI and MI distinguish between the nicotinic acceptlcholine receptor agonist sites while SI does not.";
Biochemistry 33:14058-14063(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kobayashi Y., Ohkubo T., Kyogoku Y., Nishiuchi Y., Sakakibara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gray W.R., Luque F.A., Galyean R., Atherton E., Sheppard R.C., Stone B.L., Reyes A., Alford J., McIntosh M., Olivera B.M., Cruz L.J., Rivier J.; "Conotoxin GI: disulfide bridges, synthesis, and preparation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96378624; PubMed-8784187; Guddat L.W., Martin J.A., Shan L., Edmundson A.B., Gray W.R., "Three-dimensional structure of the alpha-conotoxin GI at 1.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nishluchi Y., Sakakibara S.; "Primary and secondary structure of conotoxin GI, a neurotoxic tridecapeptide from a marine snail."; FEBS Lett. 148:260-262(1982).
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Pardi A., Galdes A., Florance J., Maniconte D.;
"Solution structures of alpha-conotoxin Gl determined by two-
                                                                                                                                                                                                                                                                                                      Gray W.R., Luque F.A., Olivera B.M., Barrett J., Cruz L.J.; "Peptide toxins from Conus geographus venom."; J. Biol. Chem. 256:4734-4740(1981).
                                                                 Conus geographus (Geography cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPARISON WITH ALPHA-CONOTOXIN SI AND ALPHA-CONOTOXIN MI
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-conotoxin GIA [Contains: Alpha-conotoxin GI (G1)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (1.2 ANGSTROMS) OF GI.
                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFIDE BONDS OF GI, AND SYNTHESIS OF GI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding sites of nicotinic receptors."; Mol. Pharmacol. 48:105-111(1995).
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                                                                                                                                                                                                                                                                         MEDLINE-81191854; PubMed-7014556;
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Biochemistry 28:5494-5501(1989).
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                                                                                                                                                                       NCBI_TaxID=6491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=6466616;
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                                                                                                                                                                                                                                                                                        "NMR solution conformation of an antitoxic analogue of alpha-conotoxin
GI: identification of a common nicotinic acetylcholine receptor
alpha(1)-subunit binding surface for small ligands and alpha-
conotoxins.",
                                                                                                                                                                                                                                                                                                                                                                        -I. FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them. The higher affinity site for alpha-conotoxin GI is the alpha/delta site on mouse muscle-deriverd BG3H-1 receptor, and the other site (alpha/gamma site) on nicotinic receptors from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Expressed by the venom duct.
-1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R->A: REDUCTION IN AFFINITY FOR BOTH
ALPHA/DELTA AND ALPHA/GAMMA SITES ON
BC3H-1 RECEPORS AND LOSS OF AFFINITY FOR
BOTH ALPHA/DELTA AND ALPHA/GAMMA SITES ON
                              Maslennikov I.V., Sobol A.G., Gladky K.V., Lugovskoy A.A.,
Ostrovsky A.G., Tsetlin V.I., Ivanov V.T., Arseniev A.S.;
"Two distinct structures of dlpha-conotoxin GI in aqueous solution.";
Eur. J. Biochem. 254:238-247(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                             Gehrmann J., Alewood P.F., Craik D.J., "Structure determination of the three disulfide bond isomers of alpha-conotoxin GI: a model for the role of disulfide bonds in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acetylcholine receptor inhibitor; Amidation; 3D-structure. PEPTIDE 1 15 ALPHA-CONOTOXIN GIA. PEPTIDE 1 13 ALPHA-CONOTOXIN GI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 1; Length 15;
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2AE73EE90F8C2E19 CRC64;
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                                                                                                                                                                                                                                            STRUCTURE BY NMR OF AN ANTITOXIC ANALOG OF GI.
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01-FEB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA terminal protein (Protein GP3) (Fragment).
3 OR E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Postsynaptic neurotoxin; Neurotoxin; Toxin;
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Torpedo californica electric organ.
                                                                                                                                                                                                                                                              MEDLINE=99438341; PubMed=10508392;
                                                                                                                                                                                                                                                                                                                                                           Biochemistry 38:11895-11904(1999).
                                                                                                                               MEDLINE=98239743; PubMed=9571060;
                                                                                                                                                                                                              Mol. Biol. 278:401-415(1998).
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STRUCTURE BY NMR OF GI. PubMed=9660176;
                                                                                                               STRUCTURE BY NMR OF GI
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1XGA; 16-FEB-99.
1XGB; 16-FEB-99.
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1QS3; 06-OCT-99.
                                                                                                                                                                                                structural stability
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                                                                                                                                                                                                                                                                               Mok K.H., Han K.H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TERM_BPM2
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9 PSGVC 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sakagami Y., Yoshida M., Isogai A., Suzuki A.;
"Peptide sex hormones inducing conjugation tube formation in compatible mating type cells of Tremella mesenterica.";
Science 212:1525-1527(1981).
-!- FUNCTION: TREMEROGEN A-13 IS PRODUCED BY THE A MATING-TYPE CELLS AND INDUCES FORMATION OF CONJUGATION TUBES IN A MATING-TYPE CELLS.
                                                                                                                                                                                                                                      -i- FUNCTION: DNA TERMINAL PROTEIN IS LINKED TO THE 5' ENDS OF BOTH STRANDS OF THE GENOME THROUGH A PHOSEHODIESTER BOND BETWEEN THE BETA-HYDROXYL GROUP OF A SERINE RESIDUE AND THE 5'-PHOSPHATE OF THE TERMINAL DEDXYADDENTATE. THIS PROTEIN IS ESSEMTIAL FOR DNA REPLICATION AND IS INVOLVED IN THE PRIMING OF DNA ELONGATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Tremella.
                                                                                                                                  Matsumoto K., Takano H., Kim C.I., Hirokawa H.; "Primary structure of bacteriophage M2 DNA polymerase: conserved segments within protein-priming DNA polymerases and DNA polymerase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                   dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.5%; Score 26; DB 1; Length 15; 50.0%; Pred. No. 2.8e+02; tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.1%; Score 23; DB 1; Length 13; 80.0%; Pred. No. 7.3e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 15 AA; 1797 MW; D3CBAFF8759DEA06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIPID 13 13 FARNESYL.
SEQUENCE 13 AA; 1204 MW; 680304A9697BA864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-NOV-1991 (Rel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Early protein; DNA replication; DNA priming;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tremella mesenterica (Jelly fungus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A01641; JTJG3.
Lipoprotein; Prenylation; Pheromone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                   MEDLINE=90128268; PubMed=2515115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Covalent protein-DNA linkage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M33144; AAA32367.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 50.0 les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                  Gene 84:247-255(1989)
                   Viruses; dsDNA viruse
phi-29-like viruses.
                                                                                                                                                                                                 of Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DRYERGDVNL 10
                                                        NCBI_TaxID=10751;
Bacteriophage M2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5217;
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P01370:
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Q
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Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C., Pernollet J.-C., Zivy M., de Vienne D.; "The maize two dimensional gel protein database: towards an integrated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Theor. Appl. Genet. 93:997-1005(1996).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.9, ITS MW IS: 34.6 kDa.
MAIRE-2DPAGE; PR0620; COLEOPTILE.
                                                                                                                                                                                                                                                  -!- FUNCTION: INHIBITS SUBTILISIN, CHYMOTRYPSIN, AND ELASTASE, BUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
                                                                                                                                                                                         Takano R., Imada C., Kamei K., Hara S.;
"The reactive site of marinostatin, a proteinase inhibitor from
marine Alteromonas sp. B-10-31".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Unknown protein from 2D-page of etiolated coleoptile (Spot 258)
                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                Score 23; DB 1; Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                         MARINOSTATIN D. PYRROLIDONE CARBOXYLIC ACID.
                       01-DBC-1992 (Rel. 24, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Marinostatin C-2 [Marinostatin C-1; Marinostatin D].
                                                                                                                                                                                                                                                                                                                                                                     6E7CEEF92EF32E44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 AA; 1564 MW; CF0BBAA0B7DE6658 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                7.9e+02;
                                                                                                                                                                                                                                                                                             MARINOSTATIN C-2.
MARINOSTATIN C-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 AA.
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                                                                                                                                                                                                                                                                                                                                                       REACTIVE BOND.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                       (strain B-10-31).
                                                                                                                                                            SEQUENCE, AND ACTIVE SITE. MEDLINE=9217615; PubMed=1794974;
                                                                                                                                                                                                                                                                                                                                                                                                  26.1%; s
                                                                                                                                                                                                                                 110:856-858(1991)
                                                                                                                                                                                                                                                                                                                                                     ACT_SITE 6 7
SEQUENCE 14 AA; 1644 MW;
                                                                                                                                                                                                                                                                             Serine protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome analysis program.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MaizeDB; 123944; -.
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Coleoptile;
                                                                                                                               NCBI_TaxID=29456;
                                                                                                                                                                                                                                                                 NOT TRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4577;
                                                                                       Alteromonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 RYPS 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RYPS 5
                                                                                                                      Alteromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UC14_MAIZE
                                                                                                                                                                                                                                      Biochem.
MARI ALTSP
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MOD_RES
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NON_TER
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DB 1; Length 15;

Score 23;

Query Match

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-i- SUBCELLULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: Expressed by the venom duct.
-i- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
                                                                                                          -!- TISSUE SPECIFICITY: Expressed by the venom duct.
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McIntosh J.M., Cruz L.J., Hunkapiller M.W., Gray W.R., Olivera B.M.; "Isolation and structure of a peptide toxin from the marine snail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
             iodinated derivatives.";
Biochemistry 23:279-6-280(21984).
-!- FUNCTION: Abar-conotoxins act on postsynaptic membranes, they
bind to the nicotinic acetylcholine receptors (nAchR) and thus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE-84032400; Pubmed-6630187; Gruz L.J., Olivera B.M.; Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.; "Conotoxin MI. Disulfide bonding and conformational states."; J. Biol. Chem. 258-12712251(1983).

-i. FUNTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                    Score 22; DB 1; Length 13; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 22; DB 1; Length 14;
Pred. No. 1.1e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                      MOD_RES 13 13 AMIDATION.
SEQUENCE 13 AA; 1422 MW; DEEE831C39297EBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION.
DEEE91898BF5E5BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUL221;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                        Postsynaptic neurotoxin; Neurotoxin; Toxin; Acetylcholine receptor inhibitor; Amidation. DISULFID 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acetylcholine receptor inhibitor; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P56973; 1B45.
Postsynaptic neurotoxin; Toxin;
                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arch. Biochem. Biophys. 218:329-334(1982).
                                                                                            -! - SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=83073458; PubMed=7149738;
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66.7%;
                                                                                                                                                                                                                                                                                                      25.0%;
                                                                                                                                                                                                                                                                                                                       50.0%;
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                                                                                                                                                                                                                                                                                                                                     3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 66.73
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha-conotoxin MI (M1).
Conus magus (Magus cone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                          PIR; A01783; NTKN2G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A01784; NTKN1M.
                                                                                                                                                                          HSSP; P56973; 1B45.
                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INHIBIT THEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                  8 CGLYYS 13
                                                                                                                                                                                                                                                                                                                                                                                                 7 CGKHFS 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 CGLYYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus magus."
                                                                             inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CXA1_CONMA
                                                                                                                                                                                                                                        DISULFID
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                     Matches
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                 δλ
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                                                                                                                                                                                                                                                                   Scomopneutes variolaris (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Diadematacea; Phymosomatoida; Stomechinidae;
                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              disulfide linkage-containing sperm-activating peptide by tandem mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECTATIONS. 179-182(1991).

-I- FUNCTION: CAUSE STIMULATION OF SPERM RESPIRATION AND MOTILITY
FIROGH INTRACELLILAR ALKALINIZATION, TRANSIENT ELEVATIONS OF
CAMP, COMP AND CLACIUM LEVELS IN SPERM CELLS, AND TRANSIENT
ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gray W.R., Luque F.A., Galyean R., Atherton E., Sheppard R.C., Stone B.L., Reyes A., Alford J., McIntosh M., Olivera B.M., Cruz L.J., Rivier J.; Rone B. Gruz L.J., Rivier J.; Ronotoxin GI: disulfide bridges, synthesis, and preparation of
                                                                                                                                                                                                                                                                                                                                                                                                               Yoshimo K.-I., Takao T., Shimonishi Y., Suzuki N.; "Determination of the amino acid sequence of an intramolecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conus geographus (Geography cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
57.1%; Pred. No. 8.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gray W.R., Luque A., Olivera B.M., Barrett J., Cruz L.J.; "Peptide toxins from Conus geographus venom."; J. Biol. Chem. 256:4734-4740(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 22; DB 1; Length 9; Pred. No. 1.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 8 8 9 AA; 1010 MW; C469B3387B076EB9 CRC64;
                                                                                                                                                                                                    01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation update)
Sperm-activating peptide (SAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                            9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Egg jelly;
MEDLINE=92097763; PubMed=1756858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=81191854; PubMed=7014556;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE, AND DISULFIDE BOND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.0%;
60.0%;
                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Conservative
                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GUANYLATE CYCLASE. PIR; S19329; S19329.
             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-conotoxin GII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID~7663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6491;
                                                            6 GNCGLYY 12
                                                                                           4 GDGGAYY 10
                                                                                                                                                                                                                                                                                                                     Stomopneustes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 PSGNC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 PEGKC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CXA2_CONGE
P01520;
                                                                                                                                                                          SAP_STOVA
P24047:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XA2_CONGE
                                                                                                                                           RESULT 7
SAP_STOVA
                              Matches
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Canis familiaris (Dog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THAN DOES BFGF.
                                                                                                                                                                                                                                                                                                                                       2 RYPSGNCGL 10
                                                                                                                                                                                                                                                                                                                                                                 | |:| |:
5 RAPNGKDGV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9615;
                          -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 LYYSSG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 LYXSNG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGF1_CANFA P18651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPCK_FASHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGF1_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPCK_FASHE
                                                                                                                                                                                                                                                                                         Matches
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δλ
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Wing M.G., Seilly D.J., Bridgman D.J., Harrison R.A.;

Wing M.G., Seilly D.J., Bridgman D.J., Harrison R.A.;

Ming M.G., Seilly D.J., Bridgman D.J., Harrison R.G., Band C.C.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
                                                                                                                                                                                                                                                                            Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cockroach Leucophaea madera: existence of N-terminally extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolation of five tachykinin-related peptides from the midgut of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
-1 TSSOB SPECIFICITY: MIDGUT.
-1 SIMILARITY: SOME SIMILARITY TO TACHYKININS.
Tachykinin; Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.9%; Score 21; DB 1; Length 9; 57.1%; Pred. No. 1.1e+05; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES 9 9 AMIDATION.
SEQUENCE 9 AA; 953 MW; 2403987699C865A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-CTT-2001 (Rel. 40, Last annotation update)
Complement Clq subcomponent, A chain (Fragment).
                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Tachykinin related peptide 4 (LemTRP 4).
                                                                                                                                                                                                                                                                                                                                               Blaberoidea; Blaberidae; Leucophaea.
NCBI_TaxID=6988;
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                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97053012; PubMed=8897641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Regul. Pept. 65:185-196(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .E., Naessel D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 PSGNCGL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PSGFMGM 8
               8 CGKNYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Midgut;
                                                                                                                                    TRP4_LEUMA
P81736;
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                                                                                                               TRP4_LEUMA
                                                                                     RESULT 10
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-:- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.
DIMER BANDS, RAT, UNLIKE HUMAN C10, CONTAINED MINOR DIMER SPECIES SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Isolation of heparin-binding growth factors from bovine, porcine and canine hearts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN, ALTHOUGH LESS STRONGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY. PIR; 803955; 803955.
Interpro; IPR002209; HB/F_growthfact.
PROSITE; PS00247; HB/F_FGF; PARTIAL.
Growth factor; Mitogen; Anglogenesis; Heparin-binding.
                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Heparin-binding growth factor 1 (HEGF-1) (Acidic fibroblast growth factor) (AfGF) (Alpha-endothelial cell growth factor) (Fragment).
                                                    InterPro; IPR001073; C1q. PROSITE; PS01113; C1Q; PARTIAL. Complement pathway; Plasma; Hydroxylation; Glycoprotein; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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1-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Putative phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32)
                                                                                                                                                                                      INTERCHAIN (WITH C-4 IN B CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quinkler W., Maasberg M., Bernotat-Danielowski S., Luethe N.,
Sharma H.S., Schaper W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.9%; Score 21; DB 1; Length 15; 66.7%; Pred. No. 1.7e+03; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                         Score 21; DB 1; Length 15; Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                  DISULFID 4 4 INTERCHAIN (WITH C-4 IN NON_TER 15 15 15 15 SEQUENCE 15 743, 1488 MW; 1B3DB000B7793955 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 15 AA; 1732 MW; 53CC9A3CADDDDAA1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89231704; PubMed=2714282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. 181:67-73(1989).
                                                                                                                                                                                                                                                                                                         23.9%;
                                                                                                                                                                                                                                                                                                                                    44.48;
                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
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                                                                                                                                              Biochem. Biophys. Res. Commun. 213:169-174(1995).
                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP]
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-ARR-1990 (Rel. 14, Created)
01-ARR-1990 (Rel. 14, Last sequence update)
01-Nov-1995 (Rel. 32, Last annotation update)
Locustatachykinin I (TK-1).
Locusta migratoria (Migratory locust).
Elvaryoda: Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Archidoidea; Orthoptera; Caelifera;
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                           Tkalcevic J., Ashman K., Meeusen E.; "Fasciola hepatica: rapid identification of newly excysted juvenile
(Phosphoenolpyruvate carboxylase) (PEPCK) (Newly excysted juvenile
                     Fasciola hepatica (Liver fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Echinostomida; Echinostomata; Fascioloidea; Fasciola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: MYOACTIVE PEPTIDE, STIMULATES THE CONTRACTION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-90184489; PubMed-2311766; Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.; "Locustatachykinin I and II, two novel insect neuropeptides with homology to peptides of the vertebrate tachykinin family."; FEBS Lett. 261:397-401(1990).
                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                    22.7%; Score 20; DB 1; Length 10; 75.0%; Pred. No. 1.7e+03; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 21.6%; Score 19; DB 1; Length 9; Local Similarity 57.1%; Pred. No. 1.1e+05; hes 4; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                          SEQUENCE 10 AA; 1069 MW; 8393A6187AA9C87A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES 9 9 AMIDATION.
SEQUENCE 9 AA, 939 MW; 2389C86B59C865A7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                           9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AA.
                                                                                                                                                                                                          InterPro: IPR000364; PEP_carboxykin. PROSITE; PS00505; PEPCK_GTP; PARTIAL. Lyase; Decarboxylase; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S08265; ECLQIM.
Tachykinin; Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                               MEDLINE=95366993; PubMed=7639732;
                                                                                                                                                                                                                                                                                                             3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                  10
             protein 1) (Fragment).
                                                                                                                                                                                                                                                                                                Local Similarity
                                                            NCBI_TaxID=6192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7004;
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                                                                                                                                                                                                                                                                                                                                     3 YPSG 6
                                                                                                                                                                                                                                                                                                                                                            1 YPDG 4
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                                                                                   SEQUENCE.
                                                                                                                                      proteins.
                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                             Matches
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ID HTF H
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Heliothis zea (Corn earworm) (Bollworm).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Helicoverpa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heliothis zea with hypertrehalosemic and adipokinetic activities.";
Biochem. Biophys. Res. Commun. 155:344-350(1988).
-!- FUNCTION: HYBERTREHALOSAEMIC FACTORS ARR NEUROPEPTIDES THAT
ELEVATE THE LEVEL OF TERHALOSE IN THE HEMOLYMPH (TREHALOSE IS
THE MAJOR CARROHYDRATE IN THE HEMOLYMPH OF INSECTS).
-!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                          Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,
Tseng C.M., Zhang Y.S., Hayes D.K.;
"Isolation and primary structure of a neuropeptide hormone from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19; Lu ...
Pred. No. 2.4e+03;
Pred. ...+ohes 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMIDATION.
8E70367865A5B9D1 CRC64;
01-AUG-1990 (Rel. 15, Created)
01-FRB-1994 (Rel. 28, Last sequence update)
01-FRB-1994 (Rel. 28, Last annotation update)
Hypertrehalosaemic hormone (HeZ-HRTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: December 2, 2002, 07:02:02 Job time : 13 secs
                                                                                                                                                                                                                                                                                                                                                 TISSUE=Corpora cardiaca;
MEDLINE=88326324; PubMed=3415690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 10 AA; 1096 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.6%;
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InterPro; IPR002047; AKH.
PROSITE; PS00256; AKH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                       NCBI_TaxID=7113;
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                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

December 2, 2002, 06:59:26; Search time 28 Seconds (without alignments) 110.382 Million cell updates/sec Run on:

US-09-902-563-18

88 1 DRYPSGNCGLYYSSG 15 Perfect score: Sedneuce:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched:

3161 tal number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 15

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SPTREMBL_21:* Database :

sp_unclassified:* sp_invertebrate:*
sp_mammal:* sp_vertebrate:* sp_rvirus:*
sp_bacteriap:* sp_organelle:* sp_archea:* sp_bacteria:* sp_rodent:* sp_plant:* sp_virus:* sp_fungi:* sp_human:* sp_mhc:* 11: 12: 13: 14: 15: 16: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

Description	+ eneitooin 88749	O8+6e9 drosophila	O8sti5 drosophila	096t78 homo sanien	Ogaive carsonella	Ogn 165 ascaris suu	O8wn04 ateles bela	Ogliwa Callia all	OUDFOA bomo sanian	095770 CVC) nra ric	Ogorad micropogoni	090703 33 33 33 3	0945cA crynthocodi	Ogune7 homo sanian	OGs8v7 +ri+ioum so	Q93uu4 escherichia
a j	P82438	Q8T6E9	Q8STI5	Q96T78	Q9AIY6	09NL65	08WP04	090WA2	000004	095770	09PRZ9	090793	094504	09UPE7	09S8V7	093004
DB	10	S	'n	4	7	Ŋ	9	13	4	œ	13	13	10	4	10	7
Query Match Length DB	10	13	13	0	11	11	10	11	15	15	15	10	12	13	15	12
% Query Match	30.7	28.4	28.4	27.3	27.3.	27.3	25.0	25.0	25.0	25.0	25.0	23.9	23.9	23.9	23.9	22.7
Score	27	25	25	24	24	24	22	22	22	22	22	21	21	21	21	20
Result No.	1	2	ĸ	4	Ŋ	9	7	∞	o	10	11	12	13	14	15	16

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13 AA.

PRT;

PRELIMINARY;

Q8T6E9

Q8T6E9 ID Q8

RESULT 2

Q9unq9 homo sapien Q9wtz6 mus musculu P82808 rattus norv Q48876 clostridium Q48872 clostridium	o murine hep homo sapien 5 lymphocyti 7 lymphocyti 9 lymphocyti	oryct homo homo homo therm	4 6 0	Q44699 Klabsiella Q9twm2 aplysia cal Q86864 lymphocytic Q86866 lymphocytic Q86868 lymphocytic Q95e14 dendrochilu
12 4 Q9UMQ9 13 11 Q9WTZ6 13 11 P82808 14 2 Q45876 14 2 Q45876	4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	00000	0 000	8 175 8
20 22.7 20 22.7 20 22.7 20 22.7 20 22.7	22222		19 21.6 18 20.5 18 20.5 18 20.5 18 20.5	
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ALIGNMENTS

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0; Gaps
                                                                                                                                     Nicotiana tabacum (Common tobacco).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                            STRAIN-CV. PETIT HAVANA;
Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
Wojtaszek P., Bolwell G.P.;
"Proteomic study of secondary cell wall proteins from transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 30.7%; Score 27; DB 10; Length 10; Best Local Similarity 66.7%; Pred. No. 4.2e+02; Matches 4; Conservative 1; Mismatches 1; Indels
                                                                  01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 10 AA; 1126 MW; C68E32486AF77B46 CRC64;
                                      10 AA.
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-!- SUBCELLULAR LOCATION: CELL WALL.
-!- TISSUE SPECIFICITY: XYLEM.
                                  PRT;
                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                        tobacco culture.
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AAL91760.1;
AAL91761.1;
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AF476784; AAL91782.1;
AF476785; AAL91783.1;
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AF476790; AAL91788.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF476793; AAL91791.1;
AF476794; AAL91792.1;
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AF476811; AAL91809.1;
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AAL91765.1;
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AAL91771.1;
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AF476787; AAL91785.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF476774; AAL91772.1;
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AAL91778.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF476804; AAL91802.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL91805.1;
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AAL91768.
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EMBL;
EMBL;
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EMBL;
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ö
                                                                                                                Drosophila miranda (Fruit fly).
Bukaryota; Metazoa; Archropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Diptera; Brachycera; Muscomorpha; Ephydroides; Drosophilldae; Drosophilla. NCBL_TaxID-7237;
                                                                                                                                                                                                                                                                                                                                  Schaeffer S.W., Goetting-Minesky M.P., Kovacevic M., Peoples J., Graybill J.L., Miller J.M., Kim K., Nelson J.G., Anderson W.W.; "Evolutionary genomics of inversions in Drosophila pseudoobscura:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schaeffer S.W., Goetting-Minesky M.P., Kovacevic M., Peoples J., Graybill J.L., Miller J.M., Kim K., Nelson J.G., Anderson W.W.; "Evolutionary genomics of inversions in Drosophila pseudoobscura:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ## MODES OF SELECTION - ;

R EMBL; AF476728; AAL91726.1; -

EMBL; AF476729; AAL91726.1; -

R EMBL; AF476730; AAL91728.1; -

R EMBL; AF476731; AAL91728.1; -

R EMBL; AF476731; AAL91729.1; -

R EMBL; AF476731; AAL91731.1; -

R EMBL; AF476734; AAL91731.1; -

R EMBL; AF476735; AAL91733.1; -

R EMBL; AF476735; AAL91733.1; -

R EMBL; AF476735; AAL91733.1; -

R EMBL; AF476736; AAL91734.1; -

R EMBL; AF476739; AAL91738.1; -

R EMBL; AF476739; AAL91739.1; -

R EMBL; AF476739; AAL91739.1; -

R EMBL; AF476743; AAL91736.1; -

R EMBL; AF476743; AAL91738.1; -

R EMBL; AF476743; AAL91740.1; -

R EMBL; AF476745; AAL91741.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.4%; Score 25; DB 5; Length 13; 80.0%; Pred. No. 1.2e+03; ative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Modes of selection.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF476817; AAL91815.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER 13 13 SEQUENCE 13 AA; 1313 MW; 15BF380B6BE05050 CRC64;
                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Myocyte enhancing factor 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Myocyte enhancing factor 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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1313 MW; 15BF380B6BE05050 CRC64;
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0; Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Atelinae; Ateles.
                                                                                                                                                                                                                                                                                                                                                       Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Bukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
Ascarididae; Ascaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Gene assignment in Ateles paniscus chamek (Platyrrhini, Primates). Allocation of 18 markers of human syntenic groups 1,2,7,14,15,17 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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Seuanez H.N., Lima C.R., Lemos B., Bonvicino C.R., Moreira M.A.M.,
Canavez F.C.;
                             Query Match 27.3%; Score 24; DB 2; Length 11; Best Local Similarity 42.9%; Pred. No. 1.5e+03; Matches 3; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 27.3%; Score 24; DB 5; Length 11; Best Local Similarity 66.7%; Pred. No. 1.5e+03; Matches 4; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.0%; Score 22; DB 6; Length 10; Best Local Similarity 75.0%; Pred. No. 2.9e+03; Matches 3; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kato Y.;
Ascaris suum asabf-delta gene, exon 2.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB029815; BAA89496.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-00T-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                                                                                11 AA.
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EMBL; AF375652; AAL31489.1; -.
                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                   ASABF-delta (Fragment).
ASABF-DELTA.
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"The human contactin-associated protein 2 (CNINAP2) spans over 2 Mb of
                                            Gaps
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EMBL, AF211138; AAK15388.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Candidatus Carsonella.
NCBL_TaxID=114186;
                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,
   28.4%; Score 25; DB 5; Length 13; 80.0%; Pred. No. 1.2e+03; tive 1; Mismatches 0; Indels
                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.3%; Score 24; DB 4; Length 9; 80.0%; Pred. No. 6.7e+05; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 11 AA; 1295 MW; 0CA993A5345B5720 CRC64;
                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
contactin-associated protein 2 (Fragment).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Appl. Environ. Microbiol. 66:2898-2905(2000).
                                                                                                                                                                                                      9 AA.
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MEDLINE=21250995; PubMed=11352571;
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MEDLINE=21125546; PubMed=11222582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA at chromosome 7q35.";
Genomics 73:108-112(2001).
EMBL; AF318295; AAK49906.1; -.
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Query Match
Best Local Similarity 80.0%
Matches 4; Conservative
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Matches 4; Conservative
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Q9AIY6
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Sites J.W. Jr., Davis S.K., Guerra T., Iverson J.B., Snell H.L.; "Character congruence and phylogenetic signal in molecular and morphological data sets: a case study in the living Iguanas (Squamata,
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Cyclura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.0%; Score 22; DB 8; Length 15; 50.0%; Pred. No. 4.4e+03; tive 2; Mismatches 2; Indels
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                                                                                                                     01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) NADH dehydrogenase subunit 4 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                         Iguanidae).";
Mol. Biol. Evol. 13:1087-1105(1996).
EMBL; U66237; AAB07473.1; -.
                                                                                                  01-FEB-1997 (TrEMBLrel. 02, Created)
                                                          PRT;
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Matches 4; Conservative
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Matches 3; Conservative
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"Single Nucleotide Polymorphism Analysis on Encoding Region of
"Single Nucleotide Polymorphism Analysis on Encoding Region of
Extracellular Fatty Acid Binding Protein Genes and Their Associations
With the Fattiness Trait in Chicken.";
Submitted (JUL.2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF402001; AAK94062.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96336021; PubMed-8757037; Mayer S.A., Rubin B.S., Sterman B.J., Byers P.H.; Mayer S.A., Rubin B.S., Sterman B.J., Byers P.H.; Spontaneous multivessel cervical artery dissection in a patient with a substitution of alanine for glycine (G13A) in the alpha 1 (I) chain of type I collagen."; Neurology 47:552-556(1996).

Demb., S83315; AAB50780.2; ---
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                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Extracellular fatty acid binding protein (Fragment).
Gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 11 AA; 1277 MW; 873417F02B187AAA CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MR-2001 (TrEMBLrel. 16, Last annotation update)
Type I collagen alpha 1(I) chain (Fragment).
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ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copeland P.A., Thomas P.; "Isolatine and evidence for two distinct "Isolation of gonadotropin subunits and evidence for two distinct gonadotropins in Aliantic croaker (Micropogonias undulatus)."; Gen. Comp. Endocrinol. 91:115-125(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22; DB 13; Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.0%; Score 22, 27.75.0%; Pred. No. 4.4e+03; rtive 0; Mismatches 1; Indels
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                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Gonadotropin 1 beta subunit (Fragment).
Micropogonias undulatus (Atlantic croaker).
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15 AA.
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PRT;
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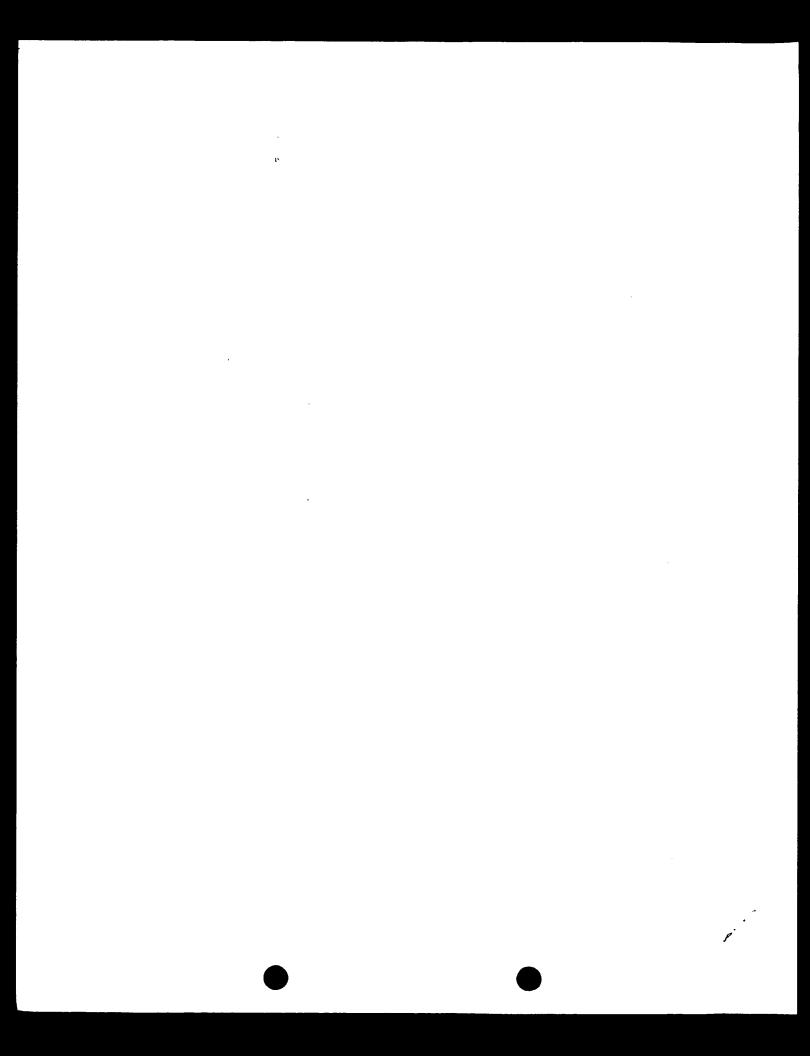
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Query Match
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Best Local Similarity
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SEQUENCE FROM N.A.
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 NCBI_TaxID=9606;
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1 ERFPS 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Crypthecodinium cohnii (Dinoflagellate).
Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Crypthecodiniaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guillebault D., Derelle E., Lozano J.C., Bingham S., Moreau H., A single TBP-like protein is present in the marine unicellular cyanism: the dinoflagellate Crypthecodinium cohnil.", Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. BMBL; AF417567; AAL15905.1; -1.
SEQUENCE 12 AA, 1299 MW; F2AE9D1D4166D051 CRC64;
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                                                                                                                                                                  Kansaku N., Nakada A., Yagi E., Okabayashi H., Guemene D.;
"Genetic variation of chicken growth hormone gene.";
Submitted (war.2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB061722; BAB69037.1;
                                                                                                                                                                                                                                                                    23.9%; Score 21; DB 13; Length 10; 66.7%; Pred. No. 4.3e+03; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.9%, Score 21; DB 10; Length 12; 75.0%, Pred. No. 5.2e+03; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                           SEQUENCE 10 AA; 1155 MW; 6841751775A40AAB CRC64;
           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                    Growth hormone (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta-tubulin (Fragment).
                                                                            Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2866;
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Q90Y93;
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Yoshikawa T., Padigaru M., Karkera J.D., Sharma M., Berrettini W.H.,
Esterling L.E., Detera-Wadleigh S.D.;
"Genomic structure and novel variants of myo-inositol monophosphatase
                                                                                                                  "A novel human myo-inositol monophatase gene, IMP.18p, maps to a susceptibility region for bipolar disorder."; Mol. Psychiatry 2:393-397(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Manoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticaea; Triticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.9%; Score 21; DB 10; Length 15; 50.0%; Pred. No. 6.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.9%; Score 21; DB 4; Length 13; 60.0%; Pred. No. 5.6e+03; ative 2; Mismatches 0; Indels
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

YOSBILKWA T., Turner G., Esterling L.E., Sanders A.R.,
Detera-Wadleigh S.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER 13 13 SEQUENCE 13 AA; 1589 MW; F3415D841F48D401 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glutenin subunits in wheat endosperm.";
Biochim. Biophys. Acta 1159:13-21(1992).
SEQUENCE 15 AA; 1559 MW; CDIA6F573C945AFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
High-molecular-weight glutenin subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Psychiatry 5:165-171(2000).
EMBL, AF025882; AAD22136.1; -
EMBL, AF025881; AAD22136.1; JOINED.
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December 2, 2002, 06:54:10 ; Search time 91 Seconds (without alignments) 21.964 Million cell updates/sec
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| SIDS2/gcgdata/geneseqy-embl/AA1989.DAT:*
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               908470 seqs, 133250620 residues
                                                                                                       OM protein - protein search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human prothrombina	Human MHC class I	Human MHC class I	Human MHC molecule	Himan MHC molecule	Human MHC molecule	Human Tak C-ensilo	Peptide EED18/47/4	Himan Tak cvolin	Purified cis-9,10-
SUMMARIES	ID	AAW88237	AAU23853	AAU24319	AAU24423	AAU24441	AAU24484	AAB26044	AAU16769		AAW23509
	DB	20	22	22	22	22	22	21	22	23	18
	Match Length DB	15	6	6	σ	6	10	12	12	12	15
* 0110	Match	100.0	37.5	37.5	37.5	37.5	37.5	37.5	37.5	37.5	37.5
	Score	88	33	33	33	33	33	33	33	33	33
Result	NO.	7	2	3	4	5	9	7	ω	6	10

Fatty acid amide h Human complementar Sequence of conoto Alpha-conotoxin pe Physarum polycepha Human complementar Hum.Cola lanuginos pH 2.5 acid phosph Hygotensive polype Amino acid sequenc Peptide derived fr Human Petil I peptide de Human mccil 14 pep Human MHC class I Human MHC class I Human MHC class I Human MHC molecule Gp IIb/IIIa recept Human ERV2 protein Fibrin polymerizat HSV-1 TK amino aci HSV-1 TK amino aci Transforming growt Peptide which is n	ucocyte myces c neous p tivatin kin-1 t
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ALIGNMENTS

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inhibitor; infection; grāft rejection; glomerulonephritis; cancēr; gastrointestinal disease; foetal loss; therapy; vaccine; epitope.
                                                                                                                         Prothrombinase; hfgl2; Fgl2; human; immune coagulation; antibody;
                                                                                                                                                                                                                                                                                                                                                                                      Modulating immune coagulation - by using Fg12 antibodies and compounds, used to treat conditions including graft rejection and
                      AAW88237 standard; Peptide; 15 AA.
                                                                                               Human prothrombinase Fg12 epitope.
                                                                                                                                                                                                                                                  98WO-CA00475.
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                                                                     15-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                              (LEVY/) LEVY G.
                                                                                                                                                                                                                                                 15-MAY-1998;
                                                                                                                                                                                                WO9851335-A1.
                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                         10-OCT-1997;
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                                                AAW88237;
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RESULT 1
             AAW88237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 103P2D6-related protein, and a ribozyme capable of cleaving a polynucleotide having the 103P2D6 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 103P2D6. The sequences can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic; gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder; single chain monoclonal antibody; cervix; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide for treating and diagnosing prostate cancer is the 103P2D6 gene which encodes for 103P2D6-related proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                               prothrombinase Fgl2 (see AAW88235). A claimed method of preventing or treating a condition requiring a reduction in immune coagulation comprises administering an inhibitor of Fgl2. The inhibitor is preferably an antibody that binds to the Fgl2 epitope. The condition to be treated in graft rejection of foetal loss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
                                                                              This peptide corresponds to amino acid residues 364-378 of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human MHC class I molecule HLA-Al binding 103P2D6 peptide #38.
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                                                                                                                                                                                                                                                                                  100.0%; Score 88; DB 20; Length 15; 100.0%; Pred. No. 1e-06;
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                                                                                                                                                                                                                                                                                                                            Mismatches
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Challita-eid PM, Faris M, Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 15; Page 81; 132pp; English.
                                       Claim 4; Page 72; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU23853 standard; Peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                 Local Similarity 100.
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                                                                                                                                                                                                                                               15 AA;
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                                                                                                                                                                                                    (claimed)
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                                                                                                                                                                                                                                                                                    Query Match
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F x 8 x 5 5 5 5 5 5 5 5 5 5 8 8 8
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peptide fragments of the polypeptide. 103P2D6 is not expressed in normal adult tissue but is aberrantly expressed in some foetal tissues and many cancers including tumours of the prostate, testis, bladder, bone, cervix, ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its related protein and also peptide fragments of the protein are therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 103P2D6-related protein, and a ribozyme capable of cleaving a polynucleotide having the 103P2D6 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 103P2D6. The sequences can be used in diagnostic methods to monitor the level of 103P2D6 gene products in serum, blood, urine and tissue and to thereby detect the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic; gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder; single chain monoclonal antibody; cervix; human.
in diagnostic methods to monitor the level of 103P2D6 gene products in
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                                                                                                                                                    Gaps
                    serum, blood, urine and tissue and to thereby detect the presence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Human MHC class I molecule HLA-B7 binding 103P2D6 peptide #4.
                                                                                                           Score 33; DB 22; Length 9;
Pred. No. 7.8e+05;
0; Mismatches 2; Indels
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Pred. No. 7.8e+05;
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                                                                                                                                                                                                                                                                                                                        AAU24319 standard; Peptide; 9 AA.
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75.0%;
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PM, Faris M,
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Best Local Similarity
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                                        cancerous cells.
                                                                             Sequence 9 AA;
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AAU24441 standard; Peptide; 9 AA.
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          Indels
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Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and adult tissue but is aberrantly expressed in some foetal tissues and many cancers including tumours of the prostate, testis, bladder, bone, cervix, ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its related protein and also peptide fragments of the protein are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that munospecifically binds to an 109P2D6-related protein, and a ribozyme capable of cleaving a polynucleotide having the 103P2D6 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 103P2D6. The sequences can be used in diagnostic methods to monitor the level of 103P2D6 gene products in carry.
                                                                                                                                                                                                        tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic; gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder; single chain monoclonal antibody; cervix; human.
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                                                                           Human MHC molecule HLA-B35 binding 103P2D6 peptide #26.
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13-JUL-2000; 2000US-0218856.
17-DEC-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-557705/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 SGNCGLYY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancerous cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SGRCGLGY 8
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Matches

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RESULT 5

WO200050460-A1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide fragments of the polypeptide. 103P206 is not expressed in normal adult tissue but is aberrantly expressed in some foetal tissues and many concers including tumours of the prostate, testis, bladder, bone, cervix, ovary, breast, pancreas, colon and lung. The 103P206 polynucleotide, its related protein and also peptide fragments of the protein are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 103P206 related protein, and a ribozyme capable of cleaving a polynucleotide having the 103P206 coding sequence, are both useful in the preparation of a composition for treating a polynucleotide having the 103P206 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 103P206. The sequences can be used in diagnostic methods to monitor the level of 103P206 gene products in serum, blood, unine and tissue and to thereby detect the presence of
                                     timour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic; gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder; single chain monoclonal antibody; cervix; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide for treating and diagnosing prostate cancer is the 103P2D6 gene which encodes for 103P2D6-related proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allergic disease; immunoprophylaxis; immunotherapy; antiallergic; immunosuppressive; vaccine; histamine release inhibitor; immunogen;
                 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
                                                                                                                                                                                                                                                                                                                                                                                           Mitchell SC, Hubert RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human IgE C-epsilon-2 PTmAb0011 peptide ligand SEQ ID NO:138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.5%; Score 33; DB 22; Length 10; 75.0%; Pred. No. 1.4e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                         DEH, Rastegar GS, Mitc
Faris M, Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 15; Page 99; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB26044 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                             26-FEB-2001; 2001WO-US05996.
                                                                                                                                                                                                                                                                                       24-FEB-2000; 2000US-0184558.
                                                                                                                                                                                                                                                                                                         13-JUL-2000; 2000US-0218856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.08
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                   (UROG-) UROGENESYS INC.
                                                                                                                                                                                                                                                                                                                                                                                           Afar DEH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-557705/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             Challita-eid PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 SGNCGLYY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancerous cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 111 1
2 SGRCGLGY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alMergy; atopy.
                                                                                                                                                             WO200162925-A2.
                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                       30-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                           Raitano AB,
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The present invention describes a peptide (I) comprising an isolated surface exposed group/epitope (EI) of C-epsilon-2 domain (D) of immunopibulin E (19b). Or its milmotope. Also described are: (1) an immunopen (II) for treating allergy comprising (I): (2) a vaccine (III) for treating allergy comprising (I): (3) a ligand (IV) capable of the paramaceutical composition (PC) comprising (IV): (5) a peptide (Ia) capable of being recognised by (IV): (6) an immunogen (II) comprising (Ia): and (7) producing (III) by producing (II): (1) com have antiallergic and immunospepressive activities, and can be used as a vaccine and histamine release inhibitor. (I), (II) and (III) are useful in medicine and in the manufacture of medicaments for treating can deventing allergies. (IV) is useful for identifying minotopes of PI, cin medicine and also in manufacturing medicaments for treating allergies. (I) is useful in diagnostics and in the affinity purification confirmating anti-igE antibodies from blood. (I), (III) and PC are consequing anti-igE antibodies from blood. (I), (III) and PC are consequing anti-igE antibodies from blood. (I), (III) and present consequences which are used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides useful for treating, preventing and ameliorating allergic diseases, comprising an isolated surface exposed group of a specific
                                                                                                                                                                                                                                                                                                                                           enwood J, Hewitt E, Lamont A, Mason S
Van Mechelen MP, Vinals De Bassols YC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; linkage technology; conjugated compound; carrier vehicle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide EED18/47/48 derived from Cepsilon2 region of human IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.5%; Score 33; DB 21; Length 12; 83.3%; Pred. No. 1.6e+02; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 7; Page 53; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU16769 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                      PEPT-) PEPTIDE THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                                                                           Greenwood J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain from immunoglobulin E -
                                22-FEB-2000; 2000WO-EP01455.
                                                                                                                                                     99GB-0018594.
                                                                       99GB-0004405.
                                                                                                                              99GB-0010538.
                                                                                                                                                                     99GB-0018603.
                                                                                                                                                                                      99GB-0021046.
99GB-0021047.
                                                                                                                                                                                                                             99GB-0025619.
                                                                                                              99GB-0010537
                                                                                                                                                                                                                                             99GB-0027698
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nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                              Turnell WG,
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-572073/53.
                                                                                                                                                                                                                                                                                                                                           Friede M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 PSGNCG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 PSGDCG 9
                                                                                                                            07-MAY-1999;
31-AUG-2000
                                                                       25-FEB-1999
                                                                                                              07-MAY-1999
                                                                                                                                                     07-AUG-1999
                                                                                                                                                                                        07-SEP-1999
                                                                                                                                                                                                          07-SEP-1999
                                                                                                                                                                                                                                               23-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                           Randall R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                            The present invention relates to linkage methodology for use in the conjugation of compounds (e.g. peptides) to carrier vehicles (e.g. macromolecules, polymers, denofrimers, proteins) to produce biological and immunological constructs. The invention provides a method for linking an epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a pharmaceutical composition or a vaccine. The invention describes peptides derived from or a minotopes of the Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E (IGB) which are used to produce conjugated compounds. The compounds or
                                                                                                                                                                                                                                                                       A linkage comprising an immunogenic conjugate useful treatment of IgE
                                                                                                                                                                                                                                                                                                                                                                                                                                compositions of the invention are useful in the manufacture of a medicament for the treatment of 1gm mediated diseases. The invention allows for controlled conjugation of a peptide epitope (antigen) to a protein so as to form an immunogenic conjugate which may be able to raise a protective antibody response in an animal or human patient. AAU16632-AAU16913 represent peptides derived from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human 1gE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
epicope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human IgE cyclic immunogenic peptide SEQ ID NO: 174.
           IgE mediated disease; antibody response.
                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                         Example 4; Page 23; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABJ00390 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; antiallergic; cyclic.
                                                                                                                                              22-FEB-2000; 2000GB-0004096. 22-AUG-2000; 2000GB-0020707.
                                                                                                              21-DEC-2000; 2000WO-GB04935.
                                                                                                                                    99GB-0030233
                                                                                                                                                                     22-AUG-2000; 2000GB-0020708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                           (ACAM-) ACAMBIS RES LTD
                                                                                                                                                                                                                            Flinn N, Johnson T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
est Local Similarity
                                                                                                                                                                                                                                                  WPI; 2001-521967/57
                                                                                                                                                                                                                                                                                   mediated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12 AA;
                                                                WO200145745-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200216409-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 PSGNCG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1||:||
4 PSGDCG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                               Homo sapiens.
                                                                                                                                    21-DEC-1999;
                                                                                        28-JUN-2001.
                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABJ00390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
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The present invention relates to conjugates suitable for use in vaccines, where the conjugate comprises a disulphide bridge cyclised peptide and an immunogenic carrier. The vaccines can be used in the treatment of allergies. The present sequence is a cyclic peptide immunogen derived from human immunoglobulin E (IgE) suitable for use in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   affinity chromatography; electric chromatography; gel filtration chromatography; ion exchange chromatography; partition chromatography; fatty acid primary amide; sleep-inducing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purified cis-9,10-octadecenoamidase internal amino acid fragment.
                                                                                                                                                                                                                                                                                                                                                                                           Conjugate for use in vaccine for treatment of allergy, comprises disulfide bridge cyclized peptide and immunogenic carrier -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Purified cis-9,10-octadeceno:amidase - useful for hydrolysing sleep-inducing fatty acid primary amide(s), and identifying inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.5%; Score 33; DB 23; Length 12; 83.3%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COase; cis-9,10-octadecenoamide; oleic acid; catalysis;
                                                                                                                                                                                                                                                                         Friede M, Mason S, Turnell WG, Vinals Bassols YC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cravatt BF, Gilula NB, Lerner RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW23509 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 78; 101pp; English.
                                                                                                                                                                                                              (PEPT-) PEPTIDE THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 13; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US10435.
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                                                       17-AUG-2001; 2001WO-EP09576.
                                                                                                               22-AUG-2000; 2000GB-0020717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibitor; soporific; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 83.39
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SCRI ) SCRIPPS RES INST.
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                                                                                                                                                                                                                                                                                                                                   WPI; 2002-489648/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 PSGNCG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 PSGDCG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-DEC-1996.
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28-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW23509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                      obtained by a chromatographic methodology selected from affinity, electric, gel filtration, ion exchange and partition chromatography. Phe Coase is characterised by enzymic activity for catalysing the conversion of cis-9,10-octadecenoamide (CO) to oleic acid and by the inclusion of an amino acid sequence fragment from rat liver Coase. The present sequence represents a specifically claimed example of such an amino acid fragment is found at residues 31 to 45 of rat liver Coase as shown in AAMIO465. The Coase can be used to catalyse the hydrolysis of fatty acid primary amides, which have sleep-inducing activity. The Coase can also be used to identify inhibitors of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             characterised by inclusion of an amino acid sequence selected from a group of 28 sequences (see AAM5784-811). These FAAHS can hydrolyse cis-9,10 octadecemonate, anandamide (arachidoyl ethanclamine), and myristic, palmitto or stearic amides. Also new are: (1) inhibiting hydrolysis of fatty acid primary amides catalysed by FAAH by FAAH inhibitor; (2) a method of screening for an CF3CO(CH2)7-CH-CH(cis)-(CH2)7Mel; and (4) nucleic acid encoding FAAH amides, particularly those in which the alkyl group has a cis unsaturation. These amides induce sleep, so FAAH can be used to study processes in which they are involved and also to develop
                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New fatty acid amide hydrolase hydrolysing soporific unsaturated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amide(s) - useful for, e.g. studying, and potentially developing
agents for modulating sleep processes
             A purified form of cis-9,10-octadecenoamidase (COase) has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cis-9,10-octadecenoamidase; fatty acid amide hydrolase; FAAH;
oleamide hydrolase; soporific; sleep.
                                                                                                                                                                                                                           37.5%; Score 33; DB 18; Length 15;
                                                                                                                                                                                                                         Score 33; ... Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fatty acid amide hydrolases (FAAHs) of the invention are
                                                                                                                                                                                                                                    55.6%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fatty acid amide hydrolase peptide (e).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gilula NB, Lerner RA;
                                                                                                                                                                                                                                                                                                                                                                              AAW57788 standard; Peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 111; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US20385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0743168.
                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-1998 (first entry)
                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-286935/25.
                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                               15 AA;
                                                                                                                                                                                                                                                                                 2 RYPSGNCGL 10
                                                                                                                                                                                                                                                                                                             1 RFPSAFCGI 9
                                                                                                                                                                  COase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9820119-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04 - NOV - 1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAY-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cravatt BF,
                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           AAW57788;
                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                      RESULT 11
x000000000000x
                                                                                                                                                                                                                                                                                                           QQ
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A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs.
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; complementary peptide; ligand; drug discovery; drug design.
                                                                                                                                             ö
                                                                                             Score 33, DB 19, Length 15, Pred. No. 2.1e+02, 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB 22; 1 Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human complementary peptide, SEQ ID NO: 2408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.2%; Sco...
100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 386; 646pp; English.
                                                                                                                                                                                                                                                                                                                                                       AAG96214 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP40328 standard; peptide; 15 AA.
                                                                                             37.5%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           drug candidates or pro-drugs
agents for modulating sleep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99GB-0029464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-DEC-2000; 2000WO-GB04776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-2001 (first entry)
                                                                                                                    Best_Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-AUG-2002 (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PROT-) PROTEOM LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-408419/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                           2 RYPSGNCGL 10
                                                  15 AA;
                                                                                                                                                                                                                    |:|| ||:
| RFPSAFCGI 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200142277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 SGNCG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 SGNCG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roberts GW,
                                                                                                                                                                                                                                                                                                                                                                                                     AAG96214;
                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP40328;
                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                   AAG96214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP40328
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27-APR-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-DEC-1996.
                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW12727;
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alpha conotoxin; inhibit; neuromuscular; synapse; signal transmission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                              The peptides of the invention are potent inhibitors of synaptic transmission at the neuromuscular junction while lacking inhibition of either nervo c muscle action potential propagation. Their action is freely reversible on dilution or removal of the peptides from the affected muscle. The peptides are useful for reversible immobilisation of a muscle or gp. of muscles in man and other vertebrates and they can be used for detection and measurement of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                 Conotoxin peptide(s) - useful for reversible immobilisation of muscles and for detecting acetyl:choline receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.2%; Score 31; DB 5; Length 15; 62.5%; Pred. No. 4.1e+02; tive 1; Mismatches 2; Indels
                                        Acetylcholine receptor; reversible immobilisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Updated on 16-AUG-2002 to add missing OS field.)
                                                                                                                            /label= Cys-S(acetamido-methyl)
                                                                                                                                              /label= Cys-S(acetamido-methyl)
                                                                                                                                                                                                                                                                                            Cruz LJ, Gray WR, Rivier JEF;
                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR75265 standard; peptide; 15 AA.
                     Sequence of conotoxin peptide GIA
                                                                                                                                                                                                                                                                                                                                                            Claim 5; column 2; 10pp; English.
                                                 synaptic transmission inhibitor.
                                                                                                                                                                 /label= Lys-NH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-conotoxin GIA peptide.
                                                                                                                                                                                                                          82US-0385125.
                                                                                                                                                                                                                                             82US-0385125.
                                                                                                                                                                                                                                                      81US-0255237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
30-JAN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   acetylcholine receptors.
                                                                                                                                                                                                                                                                          (OLIV/) OLIVERA B M.
                                                                                                                                                                                                                                                                                                              WPI; 1984-133757/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                    Conus geographus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus geographus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 CGLYYSSG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 CGRHYSCG 14
                                                                                                        Disulfide-bond
                                                                                                                                                       Modified-site
                                                                                                                   Modified-site
                                                                                                                                     Modified-site
                                                                                                                                                                                                                          04-JUN-1982;
                                                                                                                                                                                                                                             04-JUN-1982;
                                                                                                                                                                                                                                                      17-APR-1981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-DEC-1995
                                                                                                                                                                                                                                                                                           Olivera BM,
                                                                                                                                                                                    US4447356-A
                                                                                                                                                                                                       08-MAY-1984
                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR75265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR75265
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Polymerase chain reaction; PCR; primer; amplify; conotoxin; Conus; inhibitor; synaptic transmission; neuromuscular junction; sodium channel; nicotinic acetylcholine receptor; potassium channel; muscle relaxant; myasthenia gravis; small cell lung cancer; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptides all belong to a group of peptides known as the A-lineage conotoxin peptides. The A lineage conotoxin peptides have a wide variety of pharmacological uses. The A-lineage conotoxin peptides claimed (AAR75264-R75293) are useful for the inhibition of synaptic transmission at neuromuscular junctions by blocking nicotinic accept choline receptors and they also have activity against voltage-gated Na
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmission at the neuromuscular junction or are active against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The kappa-conotoxin, alpha conotoxin and alpha-like conotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cruz LJ, Hillyard DR, Mcintosh JM, Olivera BM, Santos AD;
                                                                                                                                                                                                                                                                                                        Cruz LJ, Hillyard DR, Mcintosh JM, Olivera BM, Santos AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.2%; Score 31; DB 16; Length 15; 62.5%; Pred. No. 4.1e+02; ative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              New A-lineage conotoxin peptide(s) - which inhibit synaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 4; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW12727 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          potassium or sodium channels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha-conotoxin peptide GIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                             (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93US-0084848.
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                                                                                                                         94WO-US11927.
                                                                                                                                                                                 93US-0137800.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Frace 5; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-076840/07.
                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-170189/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 CGLYYSSG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | :|| | | 7 CGRHYSCG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus geographus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and K channels.
W09511256-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUN-1993;
                                                                                                                      19-OCT-1994;
                                                                                                                                                                                 19-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
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Identifying nucleic acid encoding A-lineage conotoxin peptide(s) by amplification - uses primers corresponding to conserved regions in the signal sequence and 3'-un:translated regions, useful e.g. in treatment of small cell lung cancer

Disclosure; Column 3; 36pp; English.

AAW12726-W12769 represent conotoxin peptides. This sequence represents the GTA alpha-conotoxin peptide isolated from Conus geographus. These sequences are identified using the method of the invention. The method of the invention. The method of the invention is for identified to amplification with primer of the invention is for identified to amplification with primer sequences (see AAT59714 and AAT59715). The primers are specific for the signal sequence and 3'-untranslated (3'UTR) regions of the conotoxin of the onotoxin and the sites for detection. A-lineage conotoxins include alpha-conotoxins, and kappa-conotoxins. Alpha-conotoxins are powerful inhibitors of synaptic transmission at the neuronuscular junction, and are usually nicotinic acceptionline receptor blockers. Rappa-conotoxins are usually nicotinic acceptionline receptors blockers. Rappa-conotoxins are usually nicotinic acceptionline receptors blockers. The conotoxins identified can be used as muscle relaxants, in the diagnosis of mysathenia gravis, and for the treatment or diagnosis of small cell ung cancer. For the treatment of small cell lung cancer, the conotoxin contrinic continic/continic acceptors, and thereby blocking contininic continiis cancer in the nicotinic receptors, and thereby blocking continiis continiis cancer in the conotoxin continiis cancer in continiis cancer in continiis cancer in continiis cancer in continiis cancer continiis cancer continiis cancer continiis co 5-hydroxytryptamine.

15 AA; Sequence

0; Gaps Query Match 35.2%; Score 31; DB 18; Length 15; Best Local Similarity 62.5%; Pred. No. 4.1e+02; Matches 5; Conservative 1; Mismatches 2; Indels

8 CGLYYSSG 15 ò

QQ

Search completed: December 2, 2002, 07:01:44 Job time : 92 secs

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(without alignments)
23.886 Million cell updates/sec
                                                                                                                                                                                  December 2, 2002, 07:02:41; Search time 10 Seconds
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                  Run on:
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Gapop 10.0 , Gapext 0.5 1 DRYPSGNCGLYYSSG 15 US-09-902-563-18 88 BLOSUM62 Scoring table: Perfect score: Sequence:

pal number of hits satisfying chosen parameters:

102317 segs, 15924203 residues

Searched:

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0% Minimum DB seq length: 0 Maximum DB seq length: 15

Published_Applications_AA:*

1. /cgn2_6/ptodata/I/pubpaa/US08_NEW_PUB.pep:*

2. /cgn2_6/ptodata/I/pubpaa/PCT_NEW_PUB.pep:*

3. /cgn2_6/ptodata/I/pubpaa/US06_NEW_PUB.pep:*

4. /cgn2_6/ptodata/I/pubpaa/US07_NEW_PUB.pep:*

5. /cgn2_6/ptodata/I/pubpaa/US07_NEW_PUB.pep:*

6. /cgn2_6/ptodata/I/pubpaa/US07_NEW_PUB.pep:*

7. /cgn2_6/ptodata/I/pubpaa/US07_NEW_PUB.pep:*

7. /cgn2_6/ptodata/I/pubpaa/US07_PUBCOMB.pep:*

8. /cgn2_6/ptodata/I/pubpaa/US08_PUBCOMB.pep:*

9. /cgn2_6/ptodata/I/pubpaa/US08_PUBCOMB.pep:* /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_USCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:* beb: * /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB. Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 25, Appl	Sequence 80, Appl	4	Sequence 264, App	Sequence 32, Appl	Sequence 55, Appl	Sequence 74, Appl	Sequence 46, Appl	Sequence 14, Appl	Sequence 15, Appl	Sequence 551, App	Sequence 13, Appl	Sequence 51, Appl	Sequence 51, Appl	Sequence 5, Appli	Sequence 16, Appl	Sequence 447, App	Sequence 527, App	Sequence 634, App
ID	US-09-819-308-25	US-09-832-723-80	US-10-086-623-25	US-09-894-018-264	US-09-765-086-32	US-09-765-086-55	US-09-252-150-74	US-09-879-257A-46	US-09-758-008-14	US-09-758-008-15	US-08-424-550B-551	US-09-903-452-13	US-09-880-132-51	US-09-880-149-51	US-09-873-637-5	US-09-867-852-16	US-09-780-053-447	US-09-780-053-527	US-09-780-053-634
	10	10	6	10	10								6	10	10	10	10	10	10
Match Length DB	10	6	15	6	10	10	12	12	14	14	15	9	12	12	14	15	6	6	6
Match	39.8	30.7	30.7	30.1	29.5	29.5	29.5	29.5	29.5	29.5	29.5	28.4	28.4	28.4	28.4	28.4	27.3	27.3	27.3
Score	35	27	27	26.5	26	26	. 26	26	26	26	26	25	25	25	25	25	24	24	24
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CURRENT FILING DATE: 2001-04-11

24 27.3 14 10 US-09-78 FOR 13 Sequence 13, Appl 26 27.3 15 10 US-09-958 13 Sequence 14, Appl 27 27 27 27 3 15 10 US-09-953-510-47 Sequence 47, Appl 27 28 27 3 15 10 US-09-953-510-48 Sequence 47, Appl 29 23 26.1 15 10 US-09-958-510-49 Sequence 48, Appl 29 23 26.1 1 10 US-09-958-510-49 Sequence 14, Appl 31 23 26.1 11 10 US-09-914-704-14 Sequence 14, Appl 32 26.1 12 10 US-09-812-312-75 Sequence 17, Appl 32 26.1 12 10 US-09-812-312-75 Sequence 17, Appl 32 26.1 12 10 US-09-914-594-6 Sequence 175, Appl 34 23 26.1 14 10 US-09-914-594-6 Sequence 18, Appl 35 22 25.0 1 14 10 US-09-914-313 Sequence 37, Appl 36 22 25.0 8 10 US-09-809-5174-25 Sequence 54, Appl 41 22 25.0 9 10 US-09-898-014-3 Sequence 54, Appl 42 22 25.0 9 10 US-09-98-913-35 Sequence 54, Appl 44 22 25.0 9 10 US-09-98-913-35 Sequence 54, Appl 44 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 44 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 45 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 44 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 45 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 45 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 45 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 45 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 44 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 44 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 44 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 44 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 44 22 25.0 9 10 US-09-779-308-208 Sequence 283, Appl 44 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 44 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 44 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 44 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 44 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 44 22 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 44 25 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 44 25 25.0 9 10 US-09-779-308-206 Sequence 283, Appl 44 25 25.0 9 10 US-09-779-308-208 Sequence 283, Appl 44 25 25.0 9 10 US-09-779-308-208 Sequence 283, Appl 44 25 25.0 9 10 US-09	ALIGNMENTS
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Gaps
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APPLICANT: Tijerina, Pilar
TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
FILE REPREBUCE: GC617-2
CURRENT APPLICATION NUMBER: US/09/832,723
                                                                       GENERAL INFORMATION:
APPLICANT: No. 05200019040Aleborn, Mathieu
APPLICANT: Danen-van Oorschot, Astrid
APPLICANT: Rohn, Jennifer
TITLE OF INVENTION: AROPPILA ASSOCIATING PROTEIN
FILE REPERBNCE: 2906-4820US
CURRENT APPLICATION NUMBER: US/09/819,308
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Sequence homology analysis of AAP-5
US-09-819-308-25; Sequence 25, Application US/09819308; Patent No. US20020019040A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 80, Application US/09832723 ; Patent No. US20020098524A1
                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Estell, David A. APPLICANT: Chen, Yiyou
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CGKYYSS 9
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                                                                                                                                                                                                                                                                                                                                                        LENGTH: 10
                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 25
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30.1%; Score 26.5; DB 10; Length 9; 66.7%; Pred. No. 8.5e+04; tive 0; Mismatches 2; Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pasqualini, Renata
APPLICANT: Wadih, Arap
APPLICANT: Bredesen, Dale E.
APPLICANT: Ellerby, H. Wichael
TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
TITLE OF INVENTION: Pro-Apoptotic Activity
                                                                                                                                                                                                                                                                                                                           APPLICANT: Livingston, Brian
APPLICANT: Baker, Denisw
APPLICANT: Baker, Denisw
APPLICANT: Newman, Mark
APPLICANT: Newman, David
TITLE OF INVENTION: MRTODS AND SYSTEM FOR OPTIMIZING
TITLE OF INVENTION: MNINGENES AND PEPTIDES THEREBY
FILE REPERENCE: 39963-2003.00
CURRENT APPLICATION NUMBER: US/09/894,018
PRIOR APPLICATION NUMBER: POT/US00/35568
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR PLING DATE: 1999-12-28
PRIOR PLING DATE: 1999-12-28
PRIOR PLING DATE: 3001-04-16
NUMBER OF SEQ ID NOS: 368
SOFTHANDE: PASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Pro-Apoptotic Activity FILE REFERENCE: P-LJ 3844 CURRENT APPLICATION NUMBER: US/09/765,086 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/489,582
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEO ID NOS: 235
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                       ; Sequence 264, Application US/09894018
; Patent No. US20020119127A1
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; Patent No. US20010046498A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                Sette, Alessandro
Chestnut, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ruoslahti, Erkki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: EPIMMUNE, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: P. falciparum
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                                          11 GNCG 14
                                                                                                                                           US-09-894-018-264
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LENGTH: 10
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APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl Henrik
TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH
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                                                                                                                                                                                                                                        ; OTHER INFORMATION: peptides screened from a phage display random VS-09-882-723-80
                                                                                                                                                                                                                                                                                                                                                                                                          ;
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LOCATION: (7)..(7)

CTHER INFORMATION: can be any amino acid residue

US-10-086-623-25
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OTHER INFORMATION: can be any amino acid residue
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PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-12-8
PRIOR APPLICATION NUMBER: US 60/113,997
PRIOR APPLICATION NUMBER: US 60/150,604
PRIOR FILING DATE: 1999-08-26
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-10-05
PRIOR PELICATION NUMBER: US 60/157,756
PRIOR APPLICATION NUMBER: US 60/157,756
PRIOR PILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/197,259
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 117
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 1064/44833C2
CURRENT APPLICATION NUMBER: US/10/086,623
CURRENT FILING DATE: 2000-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/10086623 Patent No. US20020164710A1
                                                                                                                                                                                        ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: PONTEN, Annica APPLICANT: UUTELA, Marko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ERIKSSON, Ulf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AASE, Karin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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                                                                                                         SEQ ID NO 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 25
LENGTH: 15
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                     2; Indels
                                                                                                                                                                                                                                                                                APPLICANT: YAMANOTO, SACHIKO
APPLICANT: YAMANOTO, SACHIKO
APPLICANT: HANDA, TOSHIRO
APPLICANT: SHIRO, MINORU
APPLICANT: KOBATAKE, SHINZO
TITLE OF INVENTION: HYBRID BNIXMES AND USE THEREOF
TILLE PERERNCE: 55986(70281)
CURRENT APPLICATION NUMBER: US/09/879,257A
CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION.

APPLICANT: Law, Lane K.
APPLICANT: Davidson, Beverly L.
TITLE OF INVENTION: Adenovirus serotype 30 (Ad30)
FILE REPERENCE: 875.0440S1
CURRENT APPLICATION NUMBER: US/09/758,008
CURRENT FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Law, Lane K.
APPLICANT: Davidson, Beverly L.
TITLE OF INVENTION: Adenovirus serotype 30 (Ad30)
                     0; Mismatches
                                                                                                                                                                                                                   ; Sequence 46, Application US/09879257A ; Patent No. US20020081690A1
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; Patent No. US20020127721A1
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; Patent No. US20020127721A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Hepatitis B Virus
                   4; Conservative
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                  ; GENERAL INFORMATION:
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                                                               8 CGLYYS 13
                                                                                                      2 CSYYYS 7
                                                                                                                                                                                             US-09-879-257A-46
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US-09-758-008-15
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LENGTH: 14
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                     Matches
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              1; Indels
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bredesen, Dale E.
APPLICANT: Ellerby, H. Michael
TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
TITLE OF INVENTION: Pro-Apportic Activity
FILE REFERENCE: P-LJ 3844
CURRENT APPLICATION NUMBER: US/09/765,086
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US 09/489,582
MINDER OF STELLING DATE: 2000-01-21
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            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/252,150A
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: US 60/075,274
EARLIER FILING DATE: 1998-02-19
EARLIER APPLICATION NUMBER: US 60/108,683
EARLIER FILING DATE: 1998-11-16
NUMBER OF SED ID NOS: 80
SOSTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 235
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: synthetic peptide US-09-765-086-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Leddetter, Jeffrey A.
APPLICANT: Hayden Ledbetter, Martha
APPLICANT: Brady, William A.
APPLICANT: Grosmaire, Laura S.
APPLICANT: Caw, Che-Leung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 74, Application US/09252150A Patent No. US20020155604A1
                                                                                                                                                                                                            ; Sequence 55, Application US/09765086
; Patent No. US20010046498A1
                                                                                                                                                                                                                                                                                                 APPLICANT: Pasqualini, Renata
APPLICANT: Wadih, Arap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                           APPLICANT: Ruoslahti, Erkki
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         4; Conservative
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                                                   5 SGNCGL 10
                                                                                5 SGNCGL 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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Matches
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TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
                                                                                                                                                                                                                      29.5%; Score 26; DB 10; Length 14; 50.0%; Pred. No. 2.8e+02; tive 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
FILE REFERENCE: 875.0440S1
CURRENT APPLICATION NUMBER: US/09/758,008
CURRENT FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 24
SOFWWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUERHOFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: POREMBSKI, PRISCILLA E. REGISTRATION NUMBER: 33,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 552
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 551: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JAMES C. ERKER
SHERI L. BUIJK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 amino acids
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                                                                                                                                                                                                                                                                   4; Conservative
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MOLECULE TYPE: protein

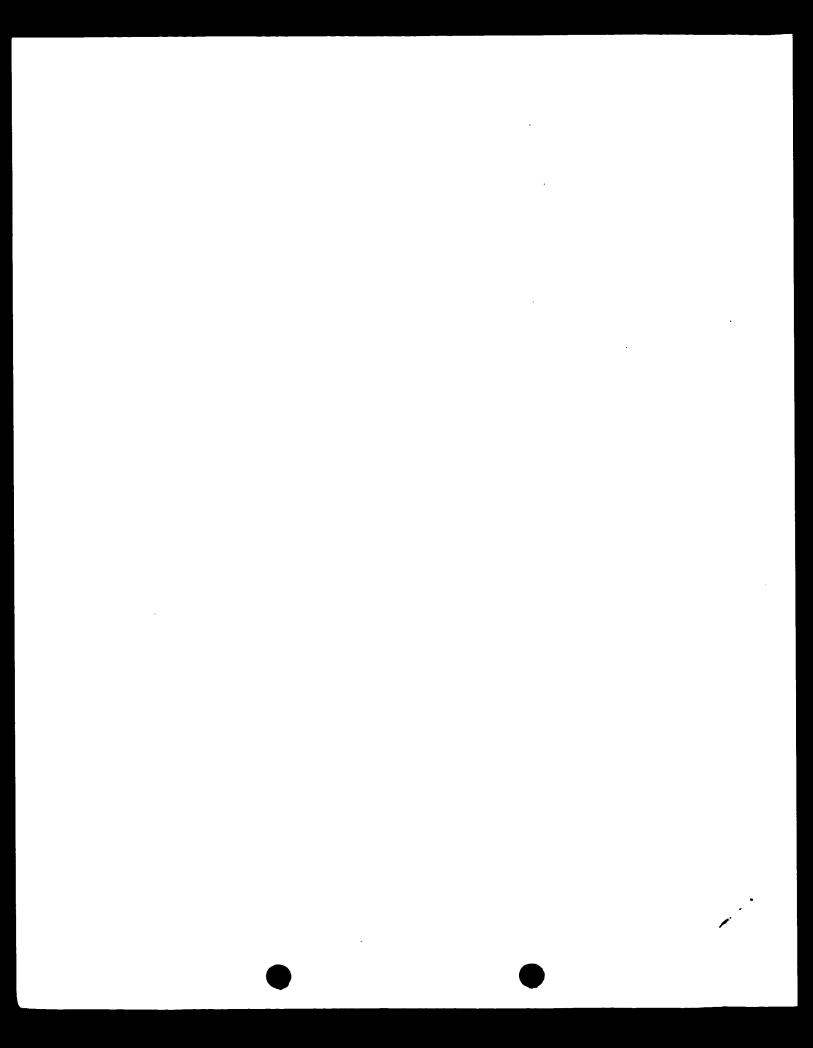
US-08-424-550B-551
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GY: linear
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US-09-758-008-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                             TYPE: PRT
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TITLE OF INVENTION: CONTROLLING PROTEIN LEVELS IN EUCARYOTIC ORGANISMS
FILE REPERENCE: 2757-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: thrombin OTHER INFORMATION: cleavage site
                                                                                           APPLICANT: Richards, Cynthia
PAPLICANT: Weiner, Michael
TITLE OF INVENTION: SYSTEM FOR GENERATING RECOMBINANT VIRUSES
FILE REFERENCE: PU34811S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.4%; Score 25; DB 10; Length 6; 80.0%; Pred. No. 8.5e+04; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/903,452
CORRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 60/084,936
PRIOR FILING DATE: 1998-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/880,132 CURRENT FILING DATE: 2001-06-14
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PRIOR APPLICATION NUMBER: 60/119,851
PRIOR FILLING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PALENLIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 51, Application US/09880132
; Patent No. US20020173049A1
; GENERAL INFORMATION:
                     ; Sequence 13, Application US/09903452; Patent No. US20020042137A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 26 SOFTWARE: Patentin Ver. 2.0
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US-09-880-132-51
US-09-903-452-13
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Sequence 51, Application US/09880149
Fatent No. US202002046843a1
GENERAL INFORMATION:
APPLICANT: Renten, John
TITLE OF INVENTION:
CURRENT PILING DATE: 1909-09-28
CURRENT PILING DATE: 1909-09-28
FILE REPERENCE: 2757-5
CURRENT APPLICATION NUMBER: 05/406,781
FRICH FILING DATE: 1999-02-12
FRICH FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 67
SEQ ID NO 51
LENGTH: 12
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TITLE OF INVENTION: THE C.MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
FILE REPERRNCE: 960296, 95131
CURRENT APPLICATION NUMBER: US/09/873,637
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 46
SOFTHARE: Patentin Ver: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.4%; Score 25; DB 10; Length 12; Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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Patent No. US20020061543A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 26.4%
Best Local Similarity 55.69
Matches 5; Conservative
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; ORCANISM: Homo sapiens
US-09-873-637-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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US-09-880-149-51
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                                                              December 2, 2002, 06:59:51 ; Search time 14 Seconds (without alignments) 31.525 Million cell updates/sec
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Sequence 6, A
Sequence 6, A
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Sequence 57,
Sequence 57,
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Sequence 6,
Sequence 6,
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Sequence 26,
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Sequence 9,
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Sequence 5,
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Sequence 65,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
            Compugen Ltd.
                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-137-800-5
US-08-477-333-5
US-08-480-750-5
US-08-690-7056-2
US-08-609-456A-57
US-08-609-456A-57
US-08-53-257A-42
US-08-53-257A-42
US-08-374-65-91
US-09-370-95-91
US-09-370-95-91
US-09-370-95-91
US-08-492-411A-20
US-08-492-411A-20
US-08-492-411A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-383-474B-26
US-08-465-391A-21
US-08-464-538B-21
US-08-463-076E-65
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compug
                                                                                                                                                                                                            al number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-442-143A-18
US-08-743-168B-9
PCT-US96-10435-9
                                                                                                                                                                                         262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                         Listing first 45 summaries
                                           OM protein - protein search, using sw model
                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                  1 DRYPSGNCGLYYSSG 15
                                                                                                                                                                                                                                                                                                                  Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                 Maximum Match 100%
                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 08
                                                                                                            US-09-902-563-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length DB
                                                                                                                                                                                                                                              Maximum DB seq length: 15
                                                                                                                                                                                                                                    nimum DB seq length: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                       Searched:
                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
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	ALIGNMENTS					
Sequence 80, Appl	US-09-270-956-80	4	15	30.7	27	45
	US-09-347-504-74	4	15	30.7	27	44
	US-09-347-504-68	4	15	30.7	27	43
	US-08-469-141A-14	e	15	30.7	27	42
Sequence 83, Appl	US-08-432-871C-83	7	12	30.7	27	41
Sequence 80, Appl	US-08-432-871C-80	7	15	30.7	27	40
Sequence 7, Appli	US-09-639-242A-7	4	14	30.7	27	39
Sequence 7, Appli	US-08-421-583-7	4	14	30.7	27	38
Sequence 7, Appli	US-08-937-228-7	4	14	30.7	27	37
Sequence 7, Appli	US-08-468-408-7	4	14	30.7	27	36
7, 1	US-08-466-468-7	-	14	30.7	27	35
	US-08-881-037-88	٣	13	30.7	27	34
Sequence 100, App	US-09-270-956-100	4	15	31.8	78	33
Sequence 55, Appl	US-09-347-504-55	4	15	31.8	58	32
100,	US-08-432-871C-100	~	15	31.8	28	31
Sequence 20, Appl	PCT-US94-07605-20	2	13	31.8	28	30
Sequence 20, Appl	US-08-089-994A-20	Н	13	31.8	28	59
Sequence 13, Appl	US-08-737-841-13	4	12	31.8	28	28
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RESULT 1
US-09-440-14A4-18
Sequence 18, Application US/09442143A
Sequence 18, Application US/09442143A
Patent No. 6403089
GENERAL INFORMATION:
APPLICANT: Levy, Gary
APPLICANT: Levy, Gary
TITLE COF INVENTION: Wethods of Modulating Immune Coagulation
TITLE REFERENCE: 9579-14
CURRENT APPLICATION NUMBER: US/09/442,143A
CURRENT APPLICATION NUMBER: US 60/046,537
PRIOR APPLICATION NUMBER: US 60/061,684
PRIOR APPLICATION NUMBER: US 60/061,684
PRIOR APPLICATION NUMBER: US 50/061,684
PRIOR APPLICATION NUMBER: US 50/061,684
SOCTWARE: PatentIn version 3.1
SEQ ID NO. 18
LENGTH: 15
TYPE: PRT
TYPE: APPLICATION NO. SAPICEN
TYPE: PRT
TYPE: APPLICATION NO. SAPICEN
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
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.; 0 100.0%; Score 88; DB 4; Length 15; 100.0%; Pred. No. 3.2e-07; 0; Indels E: The Scripps Research Institute 10550 No. 6271015th Torrey Pines Road APPLICANT: Lerner, Richard A TITLE OF INVENTION: FATTY-ACID AMIDE HYDROLASE 0; Mismatches GENERAL INFORMATION:
APPLICANT: Gilula, No. 6271015ton B
APPLICANT: Cravatt, Benjamin F Sequence 9, Application US/08743168B Patent No. 6271015 15; Conservative 1 DRYPSGNCGLYYSSG 15 1 DRYPSGNCGLYYSSG 15 CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: La Jolla California Best Local Similarity ADDRESSEE: US-08-743-168B-9 STREET: Ouerv Match CITY: Matches RESULT 2 δ

COMPUTER READABLE FORM:

92037

COUNTRY:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.5%; Score 33; DB 5; Length 15; 55.6%; Pred. No. 55; ative 2; Mismatches 2; Indels
                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: CIS-9, 10-OCTADECENOAN
WINBER OF SEQUENCES: 32
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                 APPLICATION NUMBER: US/08/743,168B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/489,535
FILING DATE: 12-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              TSRI 485.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JMBER: PCT/US96/10435
12-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/489,535
FILING DATE: 12-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 9, Application PC/TUS9610435; GENERAL INFORMATION:
                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                 NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 9:
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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Best Local Similarity
5, Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                           ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24260-104763
                                                                                                                                                                                  Conotoxin Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Maclinosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conctoxin Peptides
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                             APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Santos, Ameuriina D.
TITLE OF INVENTION: Conotoxin Pep
                     Sequence 5, Application US/08137800 Patent No. 5514774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 5, Application US/08477383
; Patent No. 5589340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 24.7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Conus geographus
                                                                                                                                                                                                                                                                                                                                                                                                                           WordPerfect 5.1
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                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                   Washington
                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
US-08-137-800-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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TELEPHONE:
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                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patchin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,383
FILING DATE: 07-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CILVER, Baldomero M. APPLICANT: Cruz, Lourdes J. APPLICANT: Hillyard, David R. APPLICANT: Macintosh, J. Michael APPLICANT: Santos, Ameurfino S. VITLE OF INVENTION: Conotoxin Peptides NUMBER OF SEQUENCES: 59 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                      24260-107673
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/137,800 FILING DATE: 19-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/487,174
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                   28,957
                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Conus geographus US-08-477-383-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEC ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                               NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 202-902 300 202-902 300 202-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                    FILING DATE: 19-OCT-1
PRIOR APPLICATION DATA:
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                    CLASSIFICATION:
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7 CGRHYSCG 14
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                         MEDIUM TYPE:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,750
ELING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                       24260-107673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24260-107673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conotoxin Peptides
                                                         APPLICATION NUMBER: US 08/084,848 FILING DATE: 29-UUN-1993 ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/137,800 FILING DATE: 19-OCT-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/084,848 FILING DATE: 29-JUN-1993 ATTORNEY/AGENT INFORMATION:
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19-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08480750; Patent No. 5633347; GENERAL INFORMATION:
                                                                                                                            NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Conus geographus
                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 62.5% Matches 5; Conservative
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                               15 amino acids
                                                                                                                                                                                                                              202-962-8300
                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: NO
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APPLICATION NUMBER: U
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                         linear
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APPLICANT:
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                  US-07-923-724-57
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                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Use of Conotoxin Peptides U002 and MII
TITLE OF INVENTION: for Treating or Detecting Small-Cell Lung Carcinoma NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07962
FILING DATE: 04-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/487,174
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-WINDOWS
                                                                                                                                                                         ORGANISM: Conus geographus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus geographus
                INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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TELEFAX: 202-962-8300
                                                                                                            .. peptide
NO
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PRIOR APPLICATION DATA:
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                                                                     amino acid
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7 CGRHYSCG 14
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                                                                                                                   MOLECULE TYPE:
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                                                                                  STRANDEDNESS
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                                                                                                                                        HYPOTHETICAL:
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                                                                                                        TOPOLOGY:
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US-08-480-750-5
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Gaps
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                                                                                                                                 APPLICANT: Torkkell, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Piddington, Christopher S.
APPLICANT: Turnon, Christopher S.
APPLICANT: Turnon, Marja K.
APPLICANT: Fagerstr m, Richard B.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.1%; Score 30; DB 1; Length 13; 55.6%; Pred. No. 1.3e+02; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                      S: Sterne, Kessler, Goldstein & Fox
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APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Miettinen-Oinonen, Arja S.K.
                                                                     APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Miettinen-Oinonen, Arja S.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1050.0240004
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FILING DATE: 19-WAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/923,724 FILING DATE: 31-JUL-1992 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-609-426A-57; Sequence 57, Application US/08609426A; Patent No. 5830733
Sequence 57, Application US/07923724; Patent No. 5780292; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: UK 8610600 FILING DATE: 30-APR-1986 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Cimbala, Michele A. REGISTRATION NUMBER: 33,851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-224
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 13 amino acids
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APPLICATION NUMBER: U
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                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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Best Local Similarity
Matches 5; Conserva
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APPLICANT: HOUSTON, CHRISTINE S.
APPLICANT: CANTRELL, MICHAEL A.
TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.1%; Score 30; DB 2; Length 13; 55.6%; Pred. No. 1.3e+02; tive 2; Mismatches 2; Indels
                                                                                                                                                  SEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.: 1100 NEW YORK AVENUE, SUITE 600 WASHINGTON
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISTITUTO DI RICERCHE DI BIOLOGIA
MOLECOLARE P. ANGELETTI S.P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/374,652C
FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 07/925,401
                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 42, Application US/08553257A ; Patent No. 5994083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Browdy and Neimark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LUZZAGO, Alessandra
NICOSIA, Alfredo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 105
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: REED, GRANT E. REGISTRATION NUMBER: 41,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MONACI, Paolo APPLICANT: CORTESE, Riccardo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FELICI, Franco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CORTESE,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 31 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ERYPSPSAG 12
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                                                                                                                                                    ADDRESSEE:
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APPLICANT:
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                                                                                                                                                                                                              STATE:
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                                                                                                                                            TITLE OF INVENTION: Production of Phytase Degrading Enzymes TITLE OF INVENTION: in Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.1%; Score 30; DB 2; Length 13; 55.6%; Pred. No. 1.3e+02; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         S: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue, Suite 600
Torkkeli, Tuula K.
Cantrell, Michael
Piddington, Christopher S.
Rambosek, John A.
Turunen, Marja K.
Fagerstr m. Richard B.
Houston, Christine S.
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PRIOR APPLICATION NUMBER: US 07/923,724
APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-UUL-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/609,426A FILING DATE: 01-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAGERSTROM, RICHARD B. MIETTINEN-OINONEN, ARJA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDDINGTON, CHRISTOPHER S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19-WAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0S 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0K 8610600
                                                                                                                                                                                                                                                                                                                                                                                                        PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEVALAINEN, HELENA K.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 30-APR-1986
ATTORNEY/AGENT INPORMATION:
NAME: Reed, Grant E.
REGISTRATION NUMBER: P-41,264
                                                                                                                                                                                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
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TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 57:
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RAMBOSEK, JOHN A.
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TOPOLOGY: hoth
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Matches 5; Conservative
                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                          STREET: 1100 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 01 CLASSIFICATION:
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US-08-374-652C-44
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    APPLICANT:
                                           APPLICANT:
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APPLICANT:
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SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                               33,963
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEREAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33,963
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                                                                                                                                                                                                                                           91:
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TELEX: 372836
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                     ATTORES AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,9
                                                   02-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 45.50
احد 5
                                                                                                                                                                                                   TELERAX: (206) 682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               LENGTH: 15 amino acids
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                 amino acid
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                                                                       CLASSIFICATION:
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                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-270-956-91
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; IDENTIFICATION METHOD: selection with specific antibodies
US-08-553-257A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.1%; Score 30; DB 2; Length 15; 83.3%; Pred. No. 1.5e+02; tive 0; Mismatches 1; Indels
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ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                               PatentIn Release #1.0, Version #1.30
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APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
LIBRARY: of recombinant peptides on phage
STREET: 419 Seventh Street N.W. Ste. 300
                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553, 257A
                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IT94/00054
FILING DATE: 05-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                         REPERENCE/DOCKET NUMBER: FELICI-1
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant protein
                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: RM93A000301
FILING DATE: 11-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 91, Application US/08432871C
Patent No. 5877010
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                     NAME: Browdy, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                         Floppy disk
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Best Local Similarity 83.3%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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                                                                                         COMPUTER READABLE FORM:
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STREET: bou
CITY: Seattle
--mr: Washington
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                                                                                                                                             OPERATING SYSTEM:
                 Washington
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STRANDEDNESS: Si
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                                                       USA
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                                                                                                           MEDIUM TYPE:
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US-08-432-871C-91
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.0%; Score 29; DB 2; Length 15; 45.5%; Pred. No. 2.2e+02; tive 1; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LOED, Lawrence A.
APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                 240052.409C1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,871C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/270,956
FILING DATE: 17-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 91, Application US/09270956 Patent No. 6451571 GENERAL INFORMATION:
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APPLICANT: Adrian V.S. Hill, et al.
TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
TITLE OF INVENTION: ANTIGENS (AS AMENDED)
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OFFRATING SYSTEM: PC-DC5/MS-DCS
SOFTWARE: WordPerfect 5.1+
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,856A
FILING DATE: October 3, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: April 3, 1992
PRIOR APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: August 20, 1992
PRIOR APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: August 20, 1992
PRIOR APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: APRIL 5, 1993
ATTORNEY/AGGNT INFORMATION:
REGISTRATION NUMBER: WO PCT/GB93/DOTICE
REGISTRATION NUMBER: WO PCT/GB93/DOTICE
REGISTRATION NUMBER: WO PCT/GB93/DOTICE
REGISTRATION NUMBER: WO PCT/GB93/DOTICE
REGISTRATION NUMBER: AD 0, 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 263-PPIR1577US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: December 2, 2002, 07:02:57
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INFORMATION FOR SEQ ID NO. 72:
SEQUENCE CHARACTERISTICS.
LENGTH: 10 amino acid residues
TYPE: amino acid STRANDEDNESS: Sin":
MOTICE TO SEGUENT OF THE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFI
                                                                                                                                                                                                                Sequence 72, Application US/08318856A Patent No. 5972351
GENERAL INFORMATION:
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1 DRYPSGNCGLY 11
                                             4 DRHPIGQTSCY 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : D.C. 
RY: U.S.A.
20006
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US-08-318-856A-72
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Job time : 15 secs

